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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:34:18 ; Search time 104.746 Seconds
(without alignments)
73.847 Million cell updates/sec

Title: US-09-780-669-114_COPY_120_139
Perfect score: 100
Sequence: 1 LLVVPKXKDYSGQEDFTQV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A. Geneseq_16Dec04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	20	4	AAM01172 Human pro
2	100	100.0	20	4	AU69817 Human pro
3	100	100.0	20	4	AAG99057 Human pro
4	100	100.0	20	4	ABU71708 Prostate
5	100	100.0	20	5	ABB95277 Epitope m
6	100	100.0	20	6	ABR54389 Prostate
7	100	100.0	20	7	ADB13972 Human pro
8	100	100.0	20	7	ADG26388 Human pro
9	100	100.0	108	2	AAV11883 Human 5'
10	100	100.0	126	2	AAV35991 Extended
11	100	100.0	126	8	ADP19299 Human sec
12	100	100.0	172	7	ADD69590 Human REM
13	100	100.0	174	8	ADP81123 Protein o
14	100	100.0	214	8	ADR65994 Human pro
15	100	100.0	214	8	ADR65994 Human pro
16	100	100.0	233	2	AAW75060 Human sec
17	100	100.0	233	6	ABO01936 Novel hum
18	100	100.0	240	4	AAAG62153 Human P50
19	100	100.0	240	5	ABB89113 Human pol
20	100	100.0	241	2	AAW69386 Prostate
21	100	100.0	241	2	AAW59954 Amino aci
22	100	100.0	241	2	AAW71870 Amino aci
23	100	100.0	241	2	AAW58380 Human sec
24	100	100.0	241	3	AAW82003 Human imm
25	100	100.0	241	3	ABG94412 Human pro

26	100	100.0	241	4	AAM01118 Human pro
27	100	100.0	241	4	AU69764 Human pro
28	100	100.0	241	4	ABW74801 Prostate
29	100	100.0	241	4	AAG99003 Human pro
30	100	100.0	241	4	ABU71654 Prostate
31	100	100.0	241	4	AAAB90679 Human ARA
32	100	100.0	241	4	AAU04962 Human ova
33	100	100.0	241	5	ABG96434 Human ova
34	100	100.0	241	5	ABB95223 Human NI-
35	100	100.0	241	5	ABG76666 Prostate
36	100	100.0	241	6	ABR54335 Prostate
37	100	100.0	241	7	ADB75601 Prostate
38	100	100.0	241	7	ADB13564 Human pro
39	100	100.0	241	7	ADG25980 Human pro
40	100	100.0	241	7	ADN39286 Cancer/an
41	100	100.0	258	5	ABG96433 Human ova
42	100	100.0	258	7	ADB75599 Prostate
43	100	100.0	273	2	AAW61618 Clone HPW
44	100	100.0	273	7	ABW01500 Human rec
45	84	84.0	241	5	ABB09512 Human TSP

ALIGNMENTS

RESULT 1
AAM01172
ID AAM01172 standard; peptide; 20 AA.

XX AC AAM01172;

XX XX 04-OCT-2001 (first entry)

DE Human prostate-specific peptide used in epitope mapping studies #29.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosolic; gene therapy; metastasis.

XX OS Homo sapiens.

XX PN WO200151633-A2.

XX PD 19-JUL-2001.

XX PF 16-JAN-2001; 2001WO-US001574.

XX PR 14-JAN-2000; 2000US-00483672.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
XX Wang A, Meagher MJ;

XX WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
XX monitoring and treating prostate cancer in a patient and for use in
XX vaccines.

XX Claim 2; Page 403; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
XX prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX and can be used in vaccine production and gene therapy. (I), (II),
XX antibodies to (II), fusion proteins comprising (II), and isolated T cells
XX prepared using (I) or (II) are used to treat cancer in a patient. (I) and
XX the antibodies are also used in the detection of cancer in a patient. The
XX cancer that is diagnosed or treated is particularly prostate cancer. (I)
XX and (II) can be used in vaccines. The antibodies or (I) can be used for
XX monitoring the progression of cancer in a patient. (I) and (II) can also
XX be used to improve diagnostic and therapeutic methods for prostate
XX cancer. They can indicate the level of metastasis as well as the prostate

The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific peptide of the invention. The peptides either represent

RESULT 4
 ABU71708
 ID ABU71708 standard; peptide; 20 AA.
 XX
 AC ABU71708;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Prostate cancer therapy associated peptide #30.
 XX
 KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KW PSMA.
 XX
 OS Homo sapiens.
 XX
 PN US2002192763-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 29-JUN-2001; 2001US-00895793.
 XX
 PR 04-OCT-1999; 99US-0157455P.
 PR 04-OCT-2000; 2000US-00679272.
 PR 28-MAR-2001; 2001US-00822827.
 XX
 (XUJJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
 PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
 XX
 DR WPI; 2001-245062/25.
 XX
 PT Prostate specific protein and its encoding polynucleotide, useful for the
 PT treatment and diagnosis of prostate cancer.
 XX
 PS Example 18; SEQ ID NO 522; 85pp; English.
 XX
 CC The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 35 sequences defined in the USPTO web
 CC site, which is encoded by any of the 4 nucleotide sequences not defined
 CC in the specification. The fusion protein, composition and methods are
 CC useful for diagnosing, preventing and/or treating cancer, particularly
 CC prostate cancer. The proteins are useful as markers to indicate the
 CC presence or absence of cancer. This is the amino acid sequence of a

CC prostate cancer therapy associated peptide. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?docID=US20020192763
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 100; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLVVPAlKKDYGSQEDFTQV 20
 Db 1 LLVVPAlKKDYGSQEDFTQV 20
 RESULT 5
 ABB95277
 ID ABB95277 standard; peptide; 20 AA.
 XX
 AC ABB95277;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Epitope mapping study peptide SEQ ID NO 522.
 XX
 KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
 KW gene therapy.
 XX
 OS Unidentified.
 XX
 PN US2002022248-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 12-JAN-2001; 2001US-00759143.
 XX
 PR 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-00904804.
 PR 10-FEB-1998; 98US-0020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00159812.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00288946.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 10-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 XX
 (XUJJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.

```
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
XX Claim 2; SEQ ID NO 522; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a
CC peptide described in the invention
XX
XX Sequence 20 AA;
SQ
Query Match 100.0%; Score 100; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLVVPAIKKDYGSQEDFTQV 20
DB 1 LLVVPAIKKDYGSQEDFTQV 20
RESULT 6
ABR54389
ID ABR54389 standard; protein; 20 AA.
XX
XX ABR54389;
AC
XX
XX 28-AUG-2003 (first entry)
DT
XX
XX Prostate tumour specific related peptide for epitope mapping SEQ ID 522.
DE
XX
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
XX immune response; prostate cancer.
XX
XX Homo sapiens.
OS
XX
XX WO200289747-A2.
PN
XX
XX 14-NOV-2002.
PD
XX
XX 09-MAY-2002; 2002WO-US014753.
PF
XX
XX 09-MAY-2001; 2001US-00852911.
PR
XX 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Poy TM, Watanabe Y;
PI Deng T;
XX
XX WPI; 2003-167130/16.
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
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PS Example 18; Page 470-471; 691pp; English.
XX
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
XX Sequence 20 AA;
SQ
Query Match 100.0%; Score 100; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLVVPAIKKDYGSQEDFTQV 20
DB 1 LLVVPAIKKDYGSQEDFTQV 20
RESULT 7
ADB13972
ID ADB13972 standard; peptide; 20 AA.
XX
XX ADB13972;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Human prostate protein P503S epitope mapping peptide #2099.
DE
XX
XX Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
XX cell therapy; vaccine; T-cell epitope;
XX class I major histocompatibility complex allele; MHC; prostate cancer;
XX tumour; antigen presenting cell; epitope.
XX
XX Homo sapiens.
OS
XX
XX US2003185830-A1.
PN
XX
XX 02-OCT-2003.
PD
XX
XX 12-NOV-2002; 2002US-00294025.
PF
XX
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
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PA (CORI-) CORIXA CORP.
XX Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
DR
XX New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
XX Example 18; Page; 101pp; English.
PS
XX The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC peptides comprise a fragment ADB13563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADB1356, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is an epitope or
CC peptide derived from one of the prostate specific proteins of the
CC invention. Note: Except where otherwise indicated, the sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030185830.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 100; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLVVPAIKDYGSQEDFTQV 20
Db 1 LLVVPAIKDYGSQEDFTQV 20
RESULT 8
ADG26388
ID ADG26388 standard; peptide; 20 AA.
XX AC ADG26388;
XX DT 26-FEB-2004 (first entry)
XX DE Human prostate-specific polypeptide #58.
XX KW Human; prostate-specific polypeptide; prostate cancer; cytostatic.
XX OS Homo sapiens.

XX US2003157089-A1.
PN 21-AUG-2003.
XX
PD 09-MAY-2002; 2002US-00144678.
PP
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 26-SEP-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.
XX 09-FEB-2001; 2001US-00780669.
XX 29-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00895814.
XX 10-DEC-2001; 2001US-00012896.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hurai J;
PI McNeill PD, Houghton RL, Vinals Y De Bassolec, Foy TM, Watanabe Y;
PI Mesagher WJ, Deng T;
XX WPI; 2003-777973/73.
XX New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
XX Example 18; SEQ ID NO 522; 99pp; English.
PS The invention relates to human prostate-specific polypeptides and the
XX polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents a human prostate-specific polypeptide of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 100; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLVVPAIKDYGSQEDFTQV 20

```
Db 1 LLVVPFAIKDYGSGEDFTQV 20
|||||
RESULT 9
AA11883
ID AAY11883 standard; protein; 108 AA.
AC AAY11883;
XX
XX
DT 18-JUN-1999 (first entry)
XX
XX
DE Human 5' EST secreted protein SEQ ID No: 483.
XX
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
forensic; gene therapy; chromosome mapping; signal peptide; prostate;
upstream regulatory sequence; cytokine activity; cell proliferation;
differentiation; haematopoiesis regulation; tissue growth regulation;
reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
thrombolytic; anti-inflammatory; tumour inhibition.
XX
XX
OS Homo sapiens.
XX
XX
PN WO9906550-A2.
XX
XX
PD 11-FEB-1999.
XX
XX
PF 31-JUL-1998; 98WO-IB001232.
XX
XX
PR 01-AUG-1997; 97US-00905144.
XX
XX
PA (GEST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
XX
DR WPI; 1999-153780/13.
XX
DR N-PSDB; AAX40605.
XX
XX
PT New isolated prostate-derived nucleic acids - used to develop products
which may have cytokine, immune regulatory, haematopoiesis regulating,
anti-inflammatory or tumour inhibition activity.
XX
XX
PS Claim 34; Page 605; 675pp; English.
XX
XX
CC AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
human secreted proteins expressed in prostate, and encode the proteins
given in AA11716 to AA11993 respectively. The proteins given represent
the signal peptide and an N-terminal fragment of a secreted protein. The
nucleic acid sequences can be used for producing secreted human gene
products. They can also be used to develop products for diagnosis and
therapy. The proteins obtained may have cytokine activity, cell
proliferation and differentiation activity, haematopoiesis regulating
activity, tissue growth regulating activity, reproductive hormone
regulating activity, chemotactic/chemokinetic activity, haemostatic and
thrombolytic activity, receptor/ligand activity, anti-inflammatory
activity, tumour inhibition activity or other activities. The products
can be used in forensic, gene therapy and chromosome mapping procedures.
The sequences can also be used for obtaining corresponding promoter
sequences. The nucleic acids encoding the signal peptides can be used for
directing extracellular secretion of a polypeptide or the insertion of a
polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ Sequence 108 AA;
Query Match 100.0%; Score 100; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 9.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLVVPFAIKDYGSGEDFTQV 20
|||||
Db 70 LLVVPFAIKDYGSGEDFTQV 89
|||||
Query Match 100.0%; Score 100; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLVVPFAIKDYGSGEDFTQV 20
|||||
Db 70 LLVVPFAIKDYGSGEDFTQV 89
|||||
RESULT 11
ADP19299
ID ADP19299 standard; protein; 126 AA.
XX
XX
AC ADP19299;
XX
XX
DT 26-AUG-2004 (first entry)
XX
```

XX human; receptor and membrane-associated protein; REMAP; cytostatic;
KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
KW thymomimetic; cell proliferative; cancer; atherosclerosis neurological;

.....

XX OS Homo sapiens.
 XX KW WO2004053079-A2.
 XX PD 24-JUN-2004.
 XX PF 08-DEC-2003; 2003WO-US038855.
 XX PR 06-DEC-2002; 2002US-0431301P.
 XX PR 06-DEC-2002; 2002US-0431321P.
 XX PR 30-JUN-2003; 2003US-0484584P.
 XX PR 07-NOV-2003; 2003US-0518607P.
 XX PA (DIAD-) DIADEXUS INC.
 XX PI Macina RA, Turner LR, Sun Y, Liu S, Chen H;
 XX DR WPI; 2004-468850/44.
 XX DR N-PSDB; ADP80988.
 XX PT New ovarian specific nucleic acid molecules and polypeptides useful for
 XX FT diagnosing, preventing or treating ovarian cancer, for producing
 XX PT transgenic animals or cells, or for research purposes.
 XX PS Claim 12; SEQ ID NO 157; 754pp; English.
 XX CC The invention relates to novel isolated nucleic acid molecules and
 XX CC polypeptides present in normal and neoplastic ovarian cells. These
 XX CC comprise a nucleic acid sequence encoding any of the 167 amino acid
 XX CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
 XX CC specification (SEQ. ID NOs: ADP81095 to ADP81261) and comprises any of
 XX CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
 XX CC in the specification (SEQ. ID NOs: ADP80967 to ADP81094). The invention
 XX CC further comprises: a method for determining the presence of an ovarian
 XX CC specific nucleic acid (OSNA) in a sample; a vector comprising the above
 XX CC nucleic acid molecule; a host cell comprising the vector; a method for
 XX CC producing a polypeptide encoded by the above nucleic acid molecule; a
 XX CC polypeptide encoded by the nucleic acid molecule cited above; an antibody
 XX CC or its fragment that specifically binds to the above polypeptide; a
 XX CC method for determining the presence of an ovarian specific protein in a
 XX CC sample; a method for diagnosing or monitoring the presence and metastases
 XX CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or
 XX CC presence of cancer in a patient; the kit comprising a means for
 XX CC determining the presence of the above nucleic acid molecule or
 XX CC polypeptide; a method of treating a patient with ovarian cancer; and a
 XX CC vaccine comprising the above polypeptide or nucleic acid encoding the
 XX CC polypeptide. The isolated nucleic acid molecules and polypeptides have
 XX CC cytostatic activity. The isolated polypeptides may be used to create a
 XX CC vaccine. The isolated nucleic acid molecules and polypeptides can be used
 XX CC for diagnosing or monitoring the presence and metastases of ovarian
 XX CC cancer and treating ovarian cancer. This sequence represents the protein
 XX CC of an ovarian specific gene of the invention.
 XX SQ Sequence 174 AA;
 Query Match 100.0%; Score 100; DB 8; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLVVPAAIKDYGSQEDFTQV 20
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 Db 8 LLVVPAAIKDYGSQEDFTQV 27
 ||||||||||||||||||
 RESULT 14
 ADR65994
 ID ADR65994 standard; protein; 214 AA.
 XX AC ADR65994;
 XX DT 02-DEC-2004 (first entry)
 XX XX

DE XX Human prostatic carcinoma derived protein SEQ ID 190 #1.
 KW human; cytostatic; diagnosis; prostatic cancer;
 XX differential expression analysis.
 OS Homo sapiens.
 XX WO2004076614-A2.
 XX PD 10-SEP-2004.
 XX PF 22-FEB-2004; 2004WO-DE000433.
 XX PR 27-FEB-2003; 2003DE-01009985.
 XX PR 14-MAY-2003; 2003DE-01022134.
 XX (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.
 XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinneemann H, Roepcke S,
 PI Xinzhong L, Staub E;
 XX WPI; 2004-653386/63.
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
 PT useful for diagnosis, treatment and in screening for specific binding
 XX agents.
 XX Claim 2; Page 585; 1607pp; German.
 XX This invention describes novel cytostatic polynucleotide and polypeptide
 CC sequences which can be used in a method for diagnosing prostatic cancer
 CC or the risk of developing prostatic cancer. Diagnosis is based on
 CC determining over transcription or over expression of the sequences in
 CC prostatic tissue. Screening for inhibitors of the sequences or detection
 CC substances involves a binding assay, any compounds that bind are
 CC selected, optionally after deconvolution of mixtures. Detection of a
 CC predetermined minimum level of the reporter indicates the presence of a
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
 CC short-interfering RNA or ribozymes; an organic molecule of molecular
 CC weight below 5000, preferably 300, that binds to the polypeptide; an
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
 CC (monoclonal) antibody directed against Ab or any of the above derivatised
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or
 CC radioisotope. The polynucleotides are identified in human prostatic
 CC cancer by differential expression analysis, using DNA microarrays,
 CC between normal and tumorous tissues, with (over)expression being detected
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from
 CC prostatic cancer patients, or subjects at risk, were incubated
 CC sequentially with anti-human CD4 murine monoclonal antibodies;
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 XX invention.
 XX SQ Sequence 214 AA;
 Query Match 100.0%; Score 100; DB 8; Length 214;
 Best Local Similarity 100.0%; Pred. No. 2e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLVVPAAIKDYGSQEDFTQV 20
 ||||||||||||||||||

Db 93 LLVPAIKDYGSQEDFTQV 112

RESULT 15

ADR66892

ID ADR66892 standard; protein; 214 AA.

XX AC ADR66892;

XX DT 02-DEC-2004 (first entry)

XX DE Human prostatic carcinoma derived DNA SEQ ID 190 #4.

XX KW human; cytostatic; diagnosis; prostatic cancer;

XX KW differential expression analysis.

XX OS Homo sapiens.

XX PN WO2004076614-A2.

XX PD 10-SEP-2004.

XX PF 22-FEB-2004; 2004WO-DE000433.

XX PR 27-FEB-2003; 2003DE-01009985.

XX PR 14-MAY-2003; 2003DE-01022134.

XX PA (HINZ/) HINZMANN B.

XX PA (DAHL/) DAHL E.

XX PA (ROSE/) ROSENTHAL A.

XX PA (HERM/) HERMANN K.

XX PA (PILA/) PILARSKY C.

XX PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;

XX PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;

XX PI Xinzhang L, Staub E;

XX DR WPI; 2004-653386/63.

XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,

XX useful for diagnosis, treatment and in screening for specific binding

XX agents.

XX Claim 2; Page 1545; 1607pp; German.

XX This invention describes novel cytostatic polynucleotide and polypeptide

XX sequences which can be used in a method for diagnosing prostatic cancer

XX or the risk of developing prostatic cancer. Diagnosis is based on

XX determining over transcription or over expression of the sequences in

XX prostatic tissue. Screening for inhibitors of the sequences or detection

XX substances involves a binding assay, any compounds that bind are

XX selected, optionally after deconvolution of mixtures. Detection of a

XX predetermined minimum level of the reporter indicates the presence of

XX tumour cells. Inhibitors can be chosen from antisense oligonucleotides,

XX short-interfering RNA or ribozymes; an organic molecule of molecular

XX weight below 5000, preferably 300, that binds to the polypeptide; an

XX aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the

XX polypeptide, preferably humanised or human; an anti-idiotypic, non-human

XX (monoclonal) antibody directed against Ab or any of the above derivatised

XX with a reporter group, cell toxin, immunostimulatory molecules and/or

XX radioisotope. The polynucleotides are identified in human prostatic

XX cancer by differential expression analysis, using DNA microarrays,

XX between normal and tumorous tissues, with (over)expression being detected

XX by quantitative PCR. Analysis of prostatic cancer samples showed that

XX CD24 was upregulated in many of them. Sections of tissue, isolated from

XX prostatic cancer patients, or subjects at risk, were incubated

XX sequentially with anti-human CD4 murine monoclonal antibodies;

XX biotinylated second antibody; streptavidin-conjugated horseradish

XX peroxidase and then diaminobenzidine as colour former (brown). The

XX samples were counterstained with hemalum (blue). Malignant cells stained

XX strongly but non-malignant cells only weakly. In 15 of 63 samples of

XX adenocarcinoma, membrane and cytoplasmic staining was very strong, and

XX lymph node metastases were also stained. ADR65805-ADR66954 represent the

CC polynucleotide and polypeptide sequences used in the method of the

CC invention.

XX

SQ Sequence 214 AA;

Query Match 100.0%; Score 100; DB 8; Length 214;

Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVPAIKDYGSQEDFTQV 20

Db 93 LLVPAIKDYGSQEDFTQV 112

Search completed: February 5, 2005, 19:59:54

Job time : 107.746 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:50:20 ; Search time 25.4237 Seconds
(without alignments)
58.724 Million cell updates/sec

Title: US-09-780-669-114_COPY_120_139

Perfect score: 100

Sequence: 1 LLVVPALKDYGSGEDFTQV 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	20	3	US-09-439-313-522
2	100	100.0	20	4	US-09-636-215-522
3	100	100.0	20	4	US-09-685-166A-522
4	100	100.0	20	4	US-09-679-426-522
5	100	100.0	20	4	US-09-759-143-522
6	100	100.0	20	4	US-09-651-236-522
7	100	100.0	233	4	US-09-148-545-137
8	100	100.0	241	3	US-08-808-148-1
9	100	100.0	241	3	US-09-020-956-114
10	100	100.0	241	3	US-09-030-607-114
11	100	100.0	241	3	US-09-439-313-114
12	100	100.0	241	3	US-09-352-616A-114
13	100	100.0	241	4	US-09-232-149A-114
14	100	100.0	241	4	US-09-159-812-114
15	100	100.0	241	4	US-09-636-215-114
16	100	100.0	241	4	US-09-685-166A-114
17	100	100.0	241	4	US-09-115-433-114
18	100	100.0	241	4	US-09-688-489-114
19	100	100.0	241	4	US-09-679-426-114
20	100	100.0	241	4	US-09-759-143-114
21	100	100.0	241	4	US-09-651-236-114
22	47	47.0	93	4	US-09-543-681A-6787
23	45	45.0	162	4	US-09-489-039A-10419
24	43.5	43.5	272	4	US-09-583-110-4023
25	43.5	43.5	277	4	US-09-107-433-3350
26	43	43.0	155	4	US-09-543-681A-7489
27	43	43.0	159	4	US-09-540-236-1985

28 43 43.0 777 4 US-09-917-254-57 Sequence 57, Appli
29 42 42.0 281 3 US-09-320-878-5 Sequence 5, Appli
30 42 42.0 281 3 US-09-105-537-43 Sequence 43, Appli
31 42 42.0 281 4 US-09-141-308-6 Sequence 6, Appli
32 42 42.0 281 4 US-09-657-440-5 Sequence 5, Appli
33 42 42.0 303 4 US-09-583-110-4065 Sequence 4065, Ap
34 42 42.0 309 4 US-09-107-433-3802 Sequence 3802, Ap
35 42 42.0 327 4 US-09-489-039A-13790 Sequence 13790, A
36 42 42.0 435 1 US-08-374-155A-5 Sequence 5, Appli
37 42 42.0 435 2 US-08-785-396-5 Sequence 5, Appli
38 42 42.0 600 1 US-08-374-155A-10 Sequence 10, Appli
39 42 42.0 600 2 US-08-785-396-10 Sequence 10, Appli
40 42 42.0 607 3 US-09-204-208A-11 Sequence 11, Appli
41 42 42.0 607 4 US-10-072-436-11 Sequence 11, Appli
42 42 42.0 629 1 US-08-374-155A-4 Sequence 4, Appli
43 42 42.0 629 2 US-08-785-396-4 Sequence 4, Appli
44 42 42.0 831 2 US-09-289-861A-8 Sequence 8, Appli
45 42 42.0 11877 3 US-09-105-537-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-439-313-522
; Sequence 522, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 522
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-439-313-522

Query Match 100.0%; Score 100; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPALKDYGSGEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LLVVPALKDYGSGEDFTQV 20

RESULT 2
US-09-636-215-522
; Sequence 522, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 522
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-636-215-522

Query Match 100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKDKYGSQEDFTQV 20
Db 1 LLVVPAAKDKYGSQEDFTQV 20

RESULT 3
US-09-685-166A-522
; Sequence 522, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 522
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-685-166A-522

Query Match 100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKDKYGSQEDFTQV 20
Db 1 LLVVPAAKDKYGSQEDFTQV 20

RESULT 4
US-09-679-426-522
; Sequence 522, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 522
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-679-426-522

Query Match 100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKDKYGSQEDFTQV 20
Db 1 LLVVPAAKDKYGSQEDFTQV 20

RESULT 5
US-09-759-143-522
; Sequence 522, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-759-143-522

Query Match 100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVWPAIKDYGSQSDFTQV 20
|||||
Db 1 LLVWPAIKDYGSQSDFTQV 20

RESULT 6
US-09-651-236-522
Sequence 522, Application US/09651236
Patent No. 6818751
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-651-236-522

Query Match 100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVWPAIKDYGSQSDFTQV 20
|||||
Db 1 LLVWPAIKDYGSQSDFTQV 20

RESULT 7
US-09-148-545-137
Sequence 137, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
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; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
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; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
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; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
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; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233

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Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVWPAKKDYGSDFTQV 20
Db 111 LLVWPAKKDYGSDFTQV 130

RESULT 8
US-08-808-148-1
; Sequence 1, Application US/08808148
; Patent No. 6020478
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer

APPLICANT: Goli, Surya
APPLICANT: Zhang, Hong Wolfe
TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,148
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0218 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT26
CLONE: 2187263
US-08-808-148-1

Query Match 100.0%; Score 100; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAlKKDYGSQEDFTQV 20
Db 120 LLVVPAlKKDYGSQEDFTQV 139

RESULT 9

US-09-020-956-114
Sequence 114, Application US/09020956
Patent No. 6261562

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 114:

SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-020-956-114

Query Match 100.0%; Score 100; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAlKKDYGSQEDFTQV 20
Db 120 LLVVPAlKKDYGSQEDFTQV 139

RESULT 10

US-09-030-607-114
Sequence 114, Application US/09030607
Patent No. 6262245

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-114

Query Match 100.0%; Score 100; DB 3; Length 241;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 120 LLVVPAAKKDYGSGEDFTQV 139

RESULT 11

US-09-439-313-114

; Sequence 114, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqui

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 114

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-439-313-114

Query Match 100.0%; Score 100; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSGEDFTQV 20
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DB 120 LLVVPAAKKDYGSGEDFTQV 139

RESULT 12

US-09-352-616A-114

; Sequence 114, Application US/09352616A

; Patent No. 6395278

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqui

; APPLICANT: Xu, Jiangchun

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.427C8

; CURRENT APPLICATION NUMBER: US/09/352,616A

; CURRENT FILING DATE: 1999-07-13

; NUMBER OF SEQ ID NOS: 472

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 114

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-352-616A-114

Query Match 100.0%; Score 100; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121-42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 114
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapien
US-09-636-215-114

Query Match 100.0%; Score 100; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAAKKDYGSQEDFTQV 20
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Db 120 LLVVPAAKKDYGSQEDFTQV 139

Search completed: February 5, 2005; 20:07:12
Job time : 34.4237 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 20:00:18 ; Search time 74.9153 Seconds
(without alignments)
86.952 Million cell updates/sec

Title: US-09-780-669-114_COPY_120_139

Perfect score: 100

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Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	100	100.0	20	9	US-09-822-827-522
4	100	100.0	20	9	US-09-895-793-522
5	100	100.0	20	9	US-09-895-814-522
6	100	100.0	20	13	US-10-012-896-522
7	100	100.0	20	14	US-10-010-940-522
8	100	100.0	20	14	US-10-144-678A-522
9	100	100.0	20	14	US-10-294-025-522
10	100	100.0	126	11	US-09-978-360A-555
11	100	100.0	233	9	US-09-981-876-137
12	100	100.0	233	10	US-09-148-545-137
13	100	100.0	240	15	US-10-264-237-1489

14	100	100.0	241	9	US-09-759-143-114
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19	100	100.0	241	9	US-09-232-880-114
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25	100	100.0	241	14	US-10-010-940-114
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27	100	100.0	241	14	US-10-144-678A-114
28	100	100.0	241	14	US-10-294-025-114
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30	100	100.0	241	15	US-10-037-417-77
31	100	100.0	241	15	US-10-037-417-78
32	100	100.0	241	16	US-10-688-838-114
33	100	100.0	258	14	US-10-097-340-324
34	100	100.0	258	14	US-10-205-823-423
35	100	100.0	273	14	US-10-156-136-20
36	84	84.0	240	9	US-09-908-193-43
37	84	84.0	240	10	US-09-823-187-74
38	84	84.0	240	15	US-10-037-417-76
39	84	84.0	241	15	US-10-037-417-22
40	62	62.0	103	11	US-09-864-408A-3062
41	47	47.0	549	15	US-10-369-493-195
42	46	46.0	102	14	US-10-317-832-48
43	46	46.0	206	15	US-10-424-599-275188
44	45	45.0	89	15	US-10-282-122A-59382
45	45	45.0	103	11	US-09-864-408A-1342

ALIGNMENTS

RESULT 1

US-09-759-143-522
; Sequence 522, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 522
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-759-143-522

Query Match 100.0%; Score 100; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSGEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LLVVPAAKKDYGSGEDFTQV 20

RESULT 2

US-09-780-669-522
; Sequence 522, Application US/09780669

; Patent No. US20020051977A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09/780,669

; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 943

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 522

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

US-09-780-669-522

Query Match 100.0%; Score 100; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSGEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LLVVPAAKKDYGSGEDFTQV 20

RESULT 3

US-09-822-827-522

; Sequence 522, Application US/09822827

; Patent No. US20020091680A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.534C1

; CURRENT APPLICATION NUMBER: US/09/822,827

; CURRENT FILING DATE: 2001-03-26

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 522

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

US-09-822-827-522

Query Match 100.0%; Score 100; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSGEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LLVVPAAKKDYGSGEDFTQV 20

RESULT 4

US-09-895-793-522

; Sequence 522, Application US/09895793

; Publication No. US20020192763A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota

; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.534C2

; CURRENT APPLICATION NUMBER: US/09/895,793

; CURRENT FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 522

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

US-09-895-793-522

Query Match 100.0%; Score 100; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSGEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LLVVPAAKKDYGSGEDFTQV 20

RESULT 5

US-09-895-814-522

; Sequence 522, Application US/09895814

; Publication No. US20020193296A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-895-814-522

Query Match 100.0%; Score 100; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAlKKDYGSQEDFTQV 20
Db 1 LLVVPAlKKDYGSQEDFTQV 20

RESULT 6
US-10-012-896-522
Sequence 522, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro

APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-10-012-896-522

Query Match 100.0%; Score 100; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAlKKDYGSQEDFTQV 20
Db 1 LLVVPAlKKDYGSQEDFTQV 20

RESULT 7
US-10-010-940-522
Sequence 522, Application US/10010940
Publication No. US20030088062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqiu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-10-010-940-522

Query Match 100.0%; Score 100; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAlKKDYGSQEDFTQV 20
Db 1 LLVVPAlKKDYGSQEDFTQV 20

RESULT 8
US-10-144-678A-522
Sequence 522, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.

```

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 522
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-144-678A-522

Query Match 100.0%; Score 100; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKKDYGSQEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LLVVPAIKKDYGSQEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |

RESULT 9
US-10-294-025-522
; Sequence 522, Application US/10294025
; Publication No. US2003018530A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 522
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-294-025-522

Query Match 100.0%; Score 100; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKKDYGSQEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LLVVPAIKKDYGSQEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |

RESULT 10
US-09-978-360A-555
; Sequence 555, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 555
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -27..-1
US-09-978-360A-555

Query Match 100.0%; Score 100; DB 11; Length 126;
Best Local Similarity 100.0%; Pred. No. 4.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKKDYGSQEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 70 LLVVPAIKKDYGSQEDFTQV 89
| | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-09-981-876-137
; Sequence 137, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; 
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1	PRIOR FILING DATE: 1997-04-11	
2	PRIOR APPLICATION NUMBER: 60/043,312	
3	PRIOR FILING DATE: 1997-04-11	
4	PRIOR APPLICATION NUMBER: 60/043,313	
5	PRIOR FILING DATE: 1997-04-11	
6	PRIOR APPLICATION NUMBER: 60/043,672	
7	PRIOR FILING DATE: 1997-04-11	
8	PRIOR APPLICATION NUMBER: 60/043,315	
9	PRIOR FILING DATE: 1997-04-11	
10	PRIOR APPLICATION NUMBER: 60/048,974	
11	PRIOR FILING DATE: 1997-06-06	
12	PRIOR APPLICATION NUMBER: 60/056,886	
13	PRIOR FILING DATE: 1997-08-22	
14	PRIOR APPLICATION NUMBER: 60/056,877	
15	PRIOR FILING DATE: 1997-08-22	
16	PRIOR APPLICATION NUMBER: 60/056,889	
17	PRIOR FILING DATE: 1997-08-22	
18	PRIOR APPLICATION NUMBER: 60/056,893	
19	PRIOR FILING DATE: 1997-08-22	
20	PRIOR APPLICATION NUMBER: 60/056,630	
21	PRIOR FILING DATE: 1997-08-22	
22	PRIOR APPLICATION NUMBER: 60/056,878	
23	PRIOR FILING DATE: 1997-08-22	
24	PRIOR APPLICATION NUMBER: 60/056,662	
25	PRIOR FILING DATE: 1997-08-22	
26	PRIOR APPLICATION NUMBER: 60/056,872	
27	PRIOR FILING DATE: 1997-08-22	
28	PRIOR APPLICATION NUMBER: 60/056,882	
29	PRIOR FILING DATE: 1997-08-22	
30	PRIOR APPLICATION NUMBER: 60/056,637	
31	PRIOR FILING DATE: 1997-08-22	
32	PRIOR APPLICATION NUMBER: 60/056,903	
33	PRIOR FILING DATE: 1997-08-22	
34	PRIOR APPLICATION NUMBER: 60/056,888	
35	PRIOR FILING DATE: 1997-08-22	
36	PRIOR APPLICATION NUMBER: 60/056,879	
37	PRIOR FILING DATE: 1997-08-22	
38	PRIOR APPLICATION NUMBER: 60/056,880	
39	PRIOR FILING DATE: 1997-08-22	
40	PRIOR APPLICATION NUMBER: 60/056,894	
41	PRIOR FILING DATE: 1997-08-22	
42	PRIOR APPLICATION NUMBER: 60/056,911	
43	PRIOR FILING DATE: 1997-08-22	
44	PRIOR APPLICATION NUMBER: 60/056,636	
45	PRIOR FILING DATE: 1997-08-22	
46	PRIOR APPLICATION NUMBER: 60/056,874	
47	PRIOR FILING DATE: 1997-08-22	
48	PRIOR APPLICATION NUMBER: 60/056,910	
49	PRIOR FILING DATE: 1997-08-22	
50	PRIOR APPLICATION NUMBER: 60/056,864	
51	PRIOR FILING DATE: 1997-08-22	
52	PRIOR APPLICATION NUMBER: 60/056,631	
53	PRIOR FILING DATE: 1997-08-22	
54	PRIOR APPLICATION NUMBER: 60/056,845	
55	PRIOR FILING DATE: 1997-08-22	
56	PRIOR APPLICATION NUMBER: 60/056,892	
57	PRIOR FILING DATE: 1997-08-22	
58	PRIOR APPLICATION NUMBER: 60/047,595	
59	PRIOR FILING DATE: 1997-03-23	
60	PRIOR APPLICATION NUMBER: 60/057,761	
61	PRIOR FILING DATE: 05-Sep-1997	
62	PRIOR APPLICATION NUMBER: 60/047,599	
63	PRIOR FILING DATE: 1997-05-23	
64	PRIOR APPLICATION NUMBER: 60/047,588	
65	PRIOR FILING DATE: 1997-05-23	
66	PRIOR APPLICATION NUMBER: 60/047,585	
67	PRIOR FILING DATE: 1997-05-23	
68	PRIOR APPLICATION NUMBER: 60/047,586	
69	PRIOR FILING DATE: 1997-05-23	
70	PRIOR APPLICATION NUMBER: 60/047,590	
71	PRIOR FILING DATE: 1997-05-23	
72	PRIOR APPLICATION NUMBER: 60/047,594	
73	PRIOR FILING DATE: 1997-05-23	

/	PRIOR APPLICATION NUMBER:	60/047,589
/	PRIOR FILING DATE:	1997-05-23
/	PRIOR APPLICATION NUMBER:	60/047,593
/	PRIOR FILING DATE:	1997-05-23
/	PRIOR APPLICATION NUMBER:	60/047,614
/	PRIOR FILING DATE:	1997-05-23
/	PRIOR APPLICATION NUMBER:	60/043,578
/	PRIOR FILING DATE:	1997-04-11
/	PRIOR APPLICATION NUMBER:	60/043,576
/	PRIOR FILING DATE:	1997-04-11
/	PRIOR APPLICATION NUMBER:	60/047,501
/	PRIOR FILING DATE:	1997-05-23
/	PRIOR APPLICATION NUMBER:	60/043,670
/	PRIOR FILING DATE:	1997-04-11
/	PRIOR APPLICATION NUMBER:	60/056,632
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,664
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,876
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,881
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,909
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,875
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,862
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,887
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,908
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/048,964
/	PRIOR FILING DATE:	1997-06-06
/	PRIOR APPLICATION NUMBER:	60/057,650
/	PRIOR FILING DATE:	1997-09-05
/	PRIOR APPLICATION NUMBER:	60/056,884
/	PRIOR FILING DATE:	1997-08-22
/	NUMBER OF SEQ ID NOS:	280
/	SOFTWARE:	Patentin Ver. 2.0
/	SEQ ID NO 137	
/	LENGTH:	233
/		
/	Query Match	100.0%; Score 100; DB 9; Length 233;
/	Best Local Similarity	100.0%; Pred. No. 9.6e-09;
/	Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
/		
/	QY	1 LLVWPAKKDYGSDFTQV 20
/		
/	DB	111 LLVWPAKKDYGSDFTQV 130
/		
/	RESULT 12	
/	US-09-148-545-137	
/	Sequence 137, Application US/09148545	
/	Publication No. US20030027132A1	
/	GENERAL INFORMATION:	
/	APPLICANT: Rosen et al.	
/	TITLE OF INVENTION: 70 Human Secreted Proteins	
/	FILE REFERENCE: PZ001P1	
/	CURRENT APPLICATION NUMBER: US/09/148,545	
/	CURRENT FILING DATE: 1998-09-04	
/	EARLIER APPLICATION NUMBER: PCT/US98/04482	
/	EARLIER FILING DATE: 1998-03-06	
/	EARLIER APPLICATION NUMBER: 60/040,162	
/	EARLIER FILING DATE: 1997-03-07	
/	EARLIER APPLICATION NUMBER: 60/040,333	
/	EARLIER FILING DATE: 1997-03-07	
/	EARLIER APPLICATION NUMBER: 60/038,621	
/	EARLIER FILING DATE: 1997-03-07	
/	EARLIER APPLICATION NUMBER: 60/040,161	
/	EARLIER FILING DATE: 1997-03-07	
/	EARLIER APPLICATION NUMBER: 60/040,626	
/	EARLIER FILING DATE: 1997-03-07	
/	EARLIER APPLICATION NUMBER: 60/040,334	
/	EARLIER FILING DATE: 1997-03-07	
/	EARLIER APPLICATION NUMBER: 60/040,336	
/	EARLIER FILING DATE: 1997-03-07	
/	EARLIER APPLICATION NUMBER: 60/040,163	
/	EARLIER FILING DATE: 1997-03-07	
/	EARLIER APPLICATION NUMBER: 60/047,615	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,600	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,597	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,502	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,633	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,583	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,617	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,618	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,503	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,592	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,581	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,584	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,500	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,587	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,492	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,598	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,613	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,582	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,596	
/	EARLIER FILING DATE: 1997-05-23	
/	EARLIER APPLICATION NUMBER: 60/047,612	

EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 05-Sep-1997
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 137
LENGTH: 233

Query Match 100.0%; Score 100; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKDYGSQEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 111 LLVVPAIKDYGSQEDFTQV 130
| | | | | | | | | | | | | | | | | | | | | |

RESULT 13
US-10-264-237-1489
Sequence 1489, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1489
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-237-1489

Query Match 100.0%; Score 100; DB 15; Length 240;
Best Local Similarity 100.0%; Pred. No. 9.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAIKDYGSQEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |

Db 119 LLVPAIKKDYGSQEDFTQV 138

RESULT 14

US-09-759-143-114
; Sequence 114, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-114

Query Match 100.0%; Score 100; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVPAIKKDYGSQEDFTQV 20
|||
Db 120 LLVPAIKKDYGSQEDFTQV 139

RESULT 15

US-09-780-669-114
; Sequence 114, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09/780,669

; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 943

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 114

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-780-669-114

Query Match 100.0%; Score 100; DB 9; Length 241;

Best Local Similarity 100.0%; Pred. No. 1e-08;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVPAIKKDYGSQEDFTQV 20

|||

Db 120 LLVPAIKKDYGSQEDFTQV 139

Search completed: February 5, 2005, 20:11:30

Job time : 75.9153 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:49:45 ; Search time 19.661 Seconds
(without alignments)
97.876 Million cell updates/sec

Title: US-09-780-669-114_COPY_120_139
Perfect score: 100
Sequence: 1 LLVVPALIKDYGSGEDFTQV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	241	2 A59262	tetraspan TSPAN-1
2	49	49.0	347	2 AC2456	hypothetical prote
3	49	49.0	764	2 B82303	conserved hypotet
4	47	47.0	89	2 AG0002	conserved hypotet
5	47	47.0	172	2 C81726	conserved hypotet
6	46	46.0	303	2 AC1087	PTS system mannose
7	45	45.0	268	2 S17446	photosystem II oxy
8	45	45.0	521	2 D88640	protein P55A8.2 [i
9	45	45.0	1274	2 T37193	enamelin matrix pr
10	44.5	44.5	248	2 S03888	photosystem II oxy
11	44.5	44.5	260	2 S10016	photosystem II oxy
12	44.5	44.5	263	2 JC5271	oxygen-evolving co
13	44.5	44.5	267	2 S00005	photosystem II oxy
14	44	44.0	92	2 H82371	conserved hypotet
15	44	44.0	402	1 E70302	molybdenum cofacto
16	44	44.0	706	2 C71929	hypothetical prote
17	43.5	43.5	272	2 D95038	PTS system, IID co
18	43.5	43.5	272	2 G97908	hypothetical prote
19	43	43.0	88	2 A46411	conserved hypotet
20	43	43.0	89	2 E91226	hypothetical prote
21	43	43.0	89	2 C86073	hypothetical prote
22	43	43.0	89	2 S40804	hypothetical prote
23	43	43.0	144	2 S23661	superoxide dismuta
24	43	43.0	222	1 DSRTN	superoxide dismuta
25	43	43.0	222	2 I57023	superoxide dismuta
26	43	43.0	303	2 AB1451	PTS system mannose
27	43	43.0	545	2 A87136	hypothetical prote
28	43	43.0	1062	2 S46367	protein kinase CDC
29	42.5	42.5	258	2 S22763	photosystem II oxy

30	42	42.0	256	2 F89955	conserved hypotet
31	42	42.0	257	2 F86697	hypothetical prote
32	42	42.0	281	2 T17413	thioesterase II (E
33	42	42.0	303	2 C97904	phosphotransferase
34	42	42.0	303	2 C95033	PTS system, mannose
35	42	42.0	360	1 A46409	alcohol dehydrogen
36	42	42.0	562	2 C82263	trehalose-6-phosph
37	42	42.0	612	2 T39684	hypothetical prote
38	41.5	41.5	257	2 G84712	hypothetical prote
39	41.5	41.5	258	1 P2T0X2	photosystem II oxy
40	41.5	41.5	596	2 T04506	hypothetical prote
41	41	41.0	89	2 AD0951	conserved hypotet
42	42	41.0	209	2 B97797	superoxide dismuta
43	41	41.0	213	2 E64568	superoxide dismuta
44	41	41.0	223	2 S48832	superoxide dismuta
45	41	41.0	223	2 S48831	superoxide dismuta

ALIGNMENTS

RESULT 1

A59262

tetraspan TSPAN-1 - human

C:Species: Homo sapiens (man)

C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C:Accession: A59262

R:Todd, S.C.; Doctor, V.S.; Levy, S.

Biochim. Biophys. Acta 1399, 101-104, 1998

A:Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.

A:Reference number: A59258; MUID:98390278; PMID:9714763

A:Accession: A59262

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-241 <TOD>

A:Cross-references: UNIPROT:O60635; GB:AF054838; NID:G2997740; PIDN:AAC69714.1; PID:G299

C:Genetics:

A:Gene: TSPAN-1

C:Superfamily: CD9 antigen

Query Match 100.0%; Score 100; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPALIKDYGSGEDFTQV 20
Db 120 LLVVPALIKDYGSGEDFTQV 139

RESULT 2

AC2456

hypothetical protein alr5203 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AC2456

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AC2456

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-347 <KUR>

A:Cross-references: UNIPROT:Q8YLU3; GB:BA000019; PIDN:BA076902.1; PID:gl17134342; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr5203

Query Match 49.0%; Score 49; DB 2; Length 347;
Best Local Similarity 52.6%; Pred. No. 3.3;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

A;Cross-references: EMBL:X58910; NID:g19895; PIDN:CAA41713.1; PID:g19896
R;Palomares, R.; Herrmann, R.G.; Oelmueller, R.
submitted to the EMBL Data Library, January 1992
A;Description: Posttranscriptional and posttranslational regulatory steps are crucial in
seedlings to white light.
A;Reference number: S44029
A;Accession: S44029
A;Molecule type: mRNA
A;Residues: 1-95, 'K', 97-175, 178-193, 'TA', 194-268 <PAL>
A;Cross-references: EMBL:X64347; NID:g417603; PIDN:CAA45699.1; PID:g417604
A;Accession: S44030
A;Molecule type: mRNA
A;Residues: 64-65, 'L', 67-69, 'S', 71-93, 'A', 95, 'T', 97-100, 'QT', 103-111, 'I', 113, 'S', 115-118
Y, 169-171, 'R', 173-175, 'S', 177-187, 'D', 189-191, 'I', 193-194, 'V', 196-200, 'AE', 203-206, 'P',
A;Cross-references: EMBL:X64348; NID:g396260; PIDN:CAA45700.1; PID:g396261
R;Takahashi, H.; Ehara, Y.; Hirano, H.
Plant Mol. Biol. 16, 689-698, 1991
A;Title: A protein in the oxygen-evolving complex in the chloroplast is associated with
A;Reference number: S14993; MUID:91329702; PMID:1868202
A;Accession: S14993
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 83-95 <PLA>
A;Accession: S14994
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 83-94 <PL2>
A;Accession: S14995
A;Molecule type: protein
A;Residues: 83-95 <PL3>
A;Experimental source: leaf
R;Hua, S.B.; Dube, S.K.; Barnett, N.M.; Kung, S.D.
Plant Mol. Biol. 18, 997-999, 1992
A;Title: Photosystem II 23 kDa polypeptide of oxygen-evolving complex is encoded by a mu
A;Reference number: S20935; MUID:92256824; PMID:1610474
A;Accession: S20936
A;Molecule type: mRNA
A;Residues: 1-9, 'H', 11-14, 'TP', 17, 'RTSLV', 'RGI', 30, 'P', 32-34, 'S', 36-38, 'L', 39-43, 'N', 44-
20-123, 'Y', 125-130, 'F', 132-136, 'A', 138-140, 'V', 142-143, 'AI', 146-155, 'F', 157-160, 'Q', 162-
09, 'Y', 211-212, 'I', 214-220, 'N', 222-228, 'VN', 231-234, 'D', 236-254, 'K', 256-260, 'T', 262-266,
A;Cross-references: EMBL:X62427; NID:g20029; PIDN:CAA44293.1; PID:g20030
A;Experimental source: clone T23-2AF
A;Accession: S22237
A;Molecule type: mRNA
A;Residues: 1-9, 'H', 11-14, 'TP', 17, 'RTSLV', 'RGI', 30, 'P', 32-34, 'S', 36-38, 'L', 39-43, 'N', 44-
20-123, 'Y', 125-130, 'F', 132-136, 'A', 138-140, 'V', 142-143, 'AI', 146-155, 'F', 157-160, 'Q', 162-
09, 'Y', 211-212, 'I', 214-220, 'N', 222-228, 'VN', 231-234, 'D', 236-254, 'K', 256-260, 'T', 262-266,
A;Cross-references: EMBL:X62426; NID:g20031; PIDN:CAA44292.1; PID:g1345550
A;Accession: S22237
A;Molecule type: mRNA
A;Residues: 1-9, 'H', 11-14, 'TP', 17, 'RTSLV', 'RGI', 30, 'P', 32-34, 'S', 36-38, 'L', 39-43, 'N', 44-
20-123, 'Y', 125-130, 'F', 132-136, 'A', 138-140, 'V', 142-143, 'AI', 146-155, 'F', 157-160, 'Q', 162-
09, 'Y', 211-212, 'I', 214-220, 'N', 222-228, 'VN', 231-234, 'D', 236-254, 'K', 256-260, 'T', 262-266,
A;Cross-references: EMBL:X62425; NID:g20002; PIDN:CAA44291.1; PID:g20003
R;Hua, S.; Dube, S.K.; Barnett, N.M.; Kung, S.
Plant Mol. Biol. 16, 749-750, 1991
A;Title: Nucleotide sequence of a cDNA clone encoding 23 kDa polypeptide of the oxygen-e
A;Reference number: S15005; MUID:91329711; PMID:1868208
A;Accession: S15005
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-9, 'H', 11-14, 'TP', 17, 'RTPLV', 'RSI', 30, 'P', 32-38, 'L', 39-46, 'A', 48-51, 'NV', 54
8-140, 'V', 142-143, 'AI', 146-155, 'F', 157-160, 'Q', 162-163, 'S', 165-167, 'Y', 169-171, 'R', 173-1
'D', 236-254, 'K', 256-260, 'T', 262-266, 'L', 268 <H04>
A;Cross-references: EMBL:X55354; NID:g19910; PIDN:CAA39039.1; PID:g19911
A;Accession: S19911
A;Gene: oee2-A
A;Introns: 88/1; 165/3; 182/3
A;Superfamily: Photosystem II oxygen-evolving complex protein 2
C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid
F;1-82/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;83-268/Product: photosystem II oxygen-evolving complex protein 2 #status predicted <MA
Query Match 45.0%; Score 45; DB 2; Length 268;
Best Local Similarity 59.1%; Pred. NO. 11;
Matches 13; Conservative 1; Mismatches 4; Indels 4; Gaps 2;

Qy 3 VVPAIKK---DYGSOEDF-TQV 20
Db 145 VTPTDKKSITDYGSPPEFLTQV 166

RESULT 8

D88640
protein F55A8.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
A;Accession: D88640
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: D88640
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-521 <STO>
A;Cross-references: GB:chr_IV; PIDN:AAC19186.1; PID:g3193148; GSPDB:GN00022; CESP:F55A8
C;Genetics:
A;Gene: F55A8.2
A;Map position: 4
C;Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide-bi

Query Match 45.0%; Score 45; DB 2; Length 521;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 6 AIKKDYGSOEDFTQV 20

Db 154 SLKKDYGDKERLAQV 168

RESULT 9

T37193
enamelin matrix protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
A;Accession: T37193
R;Hu, C.C.; Simmer, J.P.; Bartlett, J.D.; Nanci, A.; Qian, Q.; Zhang, C.; Ryu, O.H.; Xue
submitted to the EMBL Data Library, December 1996
A;Description: Cloning and characterization of mouse enamelin.
A;Reference number: Z21631
A;Accession: T37193
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1274 <HUC>
A;Cross-references: UNIPROT:O55196; EMBL:U82698; NID:g2737960; PID:g2737961; PIDN:AAB943
A;Experimental source: strain Swiss-Webster; enamel organ epithelia

Query Match 45.0%; Score 45; DB 2; Length 1274;
Best Local Similarity 42.9%; Pred. No. 59;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VVPAIKKDYGSOED 16

Db 711 ILPLPKEDYGRQDE 724

RESULT 10

S03888
Photosystem II oxygen-evolving complex protein 2 precursor - white mustard (fragment)
N;Alternate names: photosystem II extrinsic membrane protein 23K chain
C;Species: Sinapis alba (white mustard)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
A;Accession: S03888
R;Wenig, A.; Ehmann, B.; Schaefer, E.
FEBS Lett. 246, 140-144, 1989
A;Title: The 23 kDa polypeptide of the photosynthetic oxygen-evolving complex from musta
undance.

RESULT 15
 E70302
 molybdenum cofactor biosynthesis protein A - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
 C:Accession: E70302
 R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: E70302
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-402 <AQF>
 A:Cross-references: UNIPROT:O66448; GB:AE000670; GB:AE000657; NID:g2982779; PIDN:AAC0640
 A:Experimental source: strain VFS
 C:Genetics:
 A:Gene: moeA1
 C:Superfamily: Molybdenum cofactor molybdenum incorporation protein MoeA
 Query Match 44.0%; Score 44; DB 1; Length 402;
 Best Local Similarity 57.9%; Pred. No. 26;
 Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 1 LLVPAIKKDYGSQEDFTQ 19
 ||| ||| | : |||
 Db 309 LLVPAIKAMQGHREVFQ 327

Search completed: February 5, 2005, 20:05:42
 Job time : 20.661 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:36:20 ; Search time 94.9153 Seconds
(without alignments)
107.902 Million cell updates/sec

Title: US-09-780-669-114_COPY_120_139
Perfect score: 100
Sequence: 1 LLVVPFAIKKYGSOEDFTQV 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	241	1 TSNI_HUMAN	O60635 homo sapien
2	84	84.0	240	2 Q99J59	Q99J59 mus musculus
3	76	76.0	241	2 Q6AYR9	Q6AYR9 rattus norv
4	51	51.0	548	2 Q813H5	Q813H5 plasmodium
5	50.5	50.5	253	2 Q734B5	Q734B5 bacillus ce
6	49	49.0	347	2 Q8YLU3	Q8YLU3 anabaena sp
7	49	49.0	764	2 Q9KUB9	Q9KUB9 vibrio chol
8	48	48.0	173	2 Q9P919	Q9P919 pneumocysti
9	47	47.0	89	2 Q66GG7	Q66GG7 yersinia ps
10	47	47.0	89	2 Q9RB12	Q9RB12 peptobacter
11	47	47.0	89	2 Q8ZJ83	Q8ZJ83 yersinia pe
12	47	47.0	89	2 Q6DB80	Q6DB80 erwinia car
13	47	47.0	172	2 Q9PL73	Q9PL73 chlamydia m
14	46	46.0	74	2 Q8LT95	Q8LT95 lactococcus
15	46	46.0	74	2 Q7910	Q7910 lactococcus
16	46	46.0	74	2 Q9G0E7	Q9G0E7 lactococcus
17	46	46.0	107	2 Q8FD93	Q8FD93 acinetobact
18	46	46.0	303	2 Q7WYV1	Q7WYV1 streptococc
19	46	46.0	303	2 Q8YAM0	Q8YAM0 listeria mo
20	46	46.0	303	2 Q724V8	Q724V8 listeria mo
21	45.5	45.5	600	2 Q7VD65	Q7VD65 prochloroco
22	45	45.0	88	2 Q65QU5	Q65QU5 manheimia
23	45	45.0	101	1 RS24_METWA	RS24_METWA
24	45	45.0	222	2 Q6B788	Q6B788 spirometra
25	45	45.0	255	2 Q93H75	Q93H75 streptomyce
26	45	45.0	264	2 Q7VFH5	Q7VFH5 helicobacte
27	45	45.0	268	1 P8P1_TOBAC	P8P1_TOBAC
28	45	45.0	268	2 Q40457	Q40457 nicotiana t
29	45	45.0	470	2 Q688A8	Q688A8 caenorhabdi
30	45	45.0	601	2 Q7PYT9	Q7PYT9 anopheles g
31	45	45.0	737	2 Q7KPJ2	Q7KPJ2 caenorhabdi

32	45	45.0	743	2 Q688A9	Q688A9 caenorhabdi
33	45	45.0	749	2 Q8MXG7	Q8MXG7 caenorhabdi
34	45	45.0	780	2 Q76360	Q76360 caenorhabdi
35	45	45.0	1274	1 ENAM_MOUSE	ENAM_MOUSE mus musculus
36	44.5	44.5	217	1 PSBP_BRAJU	PSBP_BRAJU brassica ju
37	44.5	44.5	253	2 Q637Y5	Q637Y5 bacillus ce
38	44.5	44.5	260	1 PSBP_SINAL	PSBP_SINAL sinapis alb
39	44.5	44.5	263	1 P8P1_ARATH	P8P1_ARATH arabidopsis
40	44.5	44.5	267	1 PSBP_SPTOL	PSBP_SPTOL spinacia ol
41	44.5	44.5	294	2 Q9BLK9	Q9BLK9 bombyx mori
42	44	44.0	92	2 Q9KVV2	Q9KVV2 vibrio chol
43	44	44.0	101	1 RS24_METAC	RS24_METAC methanosarc
44	44	44.0	166	2 Q6MBI9	Q6MBI9 parachlamyd
45	44	44.0	172	2 Q9P922	Q9P922 pneumocysti

ALIGNMENTS

RESULT 1

TSNI_HUMAN
ID TSNI_HUMAN STANDARD; PRT; 241 AA.
AC O60635; O60745;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tetraspanin 1 (Tspan-1) (Tetraspanin NET-1) (Tetraspanin TM4-C).
GN Name=TSNPANI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98390278; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6;
RA Todd S.C., Doctor V.S., Levy S.;
RT "Sequences and expression of six new members of the tetraspanin/TM4SF family";
RL Biochim. Biophys. Acta 1399:101-104 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Rubinstein E., Serru V., Boucheix C.;
RT "New tetraspans identified in the EST database";
RN [3]
RP Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Puls K.L., Ni J., Liu D., Morahan G., Wright M.D.;
RT "The molecular characterization of four tetraspanins";
RN [4]
RP Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC ENBL; AF054838; AAC69714.1; -
 CC ENBL; AF065388; AAC17119.1; -
 CC ENBL; AF133425; AAF08364.1; -
 CC ENBL; BC007290; AAH07290.1; -
 CC ENBL; BC013404; AAH13404.1; -
 CC PIR; A59262; A59262.
 CC H-InvDB; HIX0000543; -
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC InterPro; IPR008952; Tetraspanin.
 CC InterPro; IPR000301; Transmem_4.
 CC Pfam; PF00335; Tetraspanin; 1.
 CC PRINTS; PR00259; TMFOUR.
 CC PROSITE; PS00421; TM4.1; FALSE_NEG.
 CC Glycoprotein; Transmembrane.
 CC DOMAIN 1 11 Cytoplasmic (Potential).
 CC TRANSMEM 12 32 Potential.
 CC DOMAIN 33 52 Extracellular (Potential).
 CC TRANSMEM 53 73 Potential.
 CC DOMAIN 74 88 Cytoplasmic (Potential).
 CC TRANSMEM 89 109 Potential.
 CC DOMAIN 110 211 Extracellular (Potential).
 CC TRANSMEM 212 232 Potential.
 CC DOMAIN 233 241 Cytoplasmic (Potential).
 CC CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 154 154 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
 CC CONFLICT 189 189 K -> E (in Ref. 1).
 CC SEQUENCE 241 AA; 26301 MW; AF938AD7147CB884 CRC64;
 SQ
 Query Match 100.0%; Score 100; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LLVPAIKDYGSGEDPTQV 20
 DB 120 LLVPAIKDYGSGEDPTQV 139
 RESULT 2
 Q99059 PRELIMINARY; PRT; 240 AA.
 AC Q99J59
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE RIKEN cDNA 9030418M05 (Mus musculus adult male colon cDNA, RIKEN full-
 DE length enriched library, clone:9030418M05 product:similar to tetraspan
 DE TSPAN-1).
 DE GN Name:9030418M05Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner C.M., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RA The FANTOM Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [6]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [7]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [8]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Koino H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yamana K. I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC003448; AAH03448.1; -;
DR EMBL; BC003448; AAC37431.1; -;
DR MGD; MGI:1914055; 9030418M05Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR00301; Transmem 4.
DR Pfam; PF00335; Tetraspanin; I.
DR PRINTS; PR00342; RHESUSRHD.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
DR PROSITE; PS00421; TM4_1; 1.
SQ SEQUENCE 240 AA; 26356 MW; AD4C448A32BC2999 CRC64;
Query Match 84.0%; Score 84; DB 2; Length 240;
Best Local Similarity 85.0%; Pred. No. 7.9e-06;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LLVPAIKDYGSQEDFTQV 20
|||||:||||:||||:
Db 120 LLVPAIKDYGYQTEFTQV 139
|||||:||||:||||:
RESULT 3
Q6AYR9 PRELIMINARY; PRT; 241 AA.
ID Q6AYR9
AC Q6AYR9
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tetraspan 1.
GN Name=MGC93753;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.N., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Tringali J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kryzinski M.I., Skalska U., Smalus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBSJ databases.

DR EMBL; BC078938; AAH78938.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR00301; Transmem 4.
DR Pfam; PF00335; Tetraspanin; I.
DR PRINTS; PR00342; RHESUSRHD.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
DR PROSITE; PS00421; TM4_1; 1.
SQ SEQUENCE 241 AA; 26453 MW; 9118B865464D1A70 CRC64;
Query Match 76.0%; Score 76; DB 2; Length 241;
Best Local Similarity 78.9%; Pred. No. 0.00019;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 2 LLVPAIKDYGSQEDFTQV 20
|||||:||||:||||:
Db 121 LLVPAIKDYGYQTEFTQV 139
|||||:||||:||||:
RESULT 4
Q8I3H5 PRELIMINARY; PRT; 548 AA.
ID Q8I3H5
AC Q8I3H5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sugar transporter, putative.
GN Name=PF01455w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
RA Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Rabbintowitsch E.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Simmonds M.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sultston J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002)
DR EMBL; AL929354; CAB51553.1; -;
SQ SEQUENCE 548 AA; 63768 MW; 245CACDS95067CF3 CRC64;
Query Match 51.0%; Score 51; DB 2; Length 548;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 1 LLVPAIKDYGSQEDFTQV 20
|||||:||||:||||:
Db . 264 ITVLVINKDYKSKEDFVQL 283
|||||:||||:||||:
RESULT 5
Q734B5 PRELIMINARY; PRT; 253 AA.
ID Q734B5
AC Q734B5

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CAX amino terminal protease family.
GN OrderedLocusNames=BCE3492;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=22523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI.1";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017275; AAS42398.1; -.
DR TIGR; BCE3492; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR003675; Abi.
DR Pfam; PF02517; Abi; 1.
KW Complete proteome; Protease.
SQ SEQUENCE 253 AA; 28985 MW; 9572AA6F36352785 CRC64;

Query Match 50.5%; Score 50.5; DB 2; Length 253;
Best Local Similarity 55.0%; Pred. No. 4.7;
Matches 11; Conservative 3; Mismatches 1; Indels 5; Gaps 1;

QY 3 VVPAI-----KKDYGSGEDF 17
   :|||  |||  |||  |||  |||
Db 48 IMPAIIAISLKKYGSQEEF 67

RESULT 6
Q8YLU3 PRELIMINARY; PRT; 347 AA.
AC Q8YLU3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alr5203 protein.
GN OrderedLocusNames=alr5203;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OC NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003599; BAB76902.1; -.
DR PIR; AC2456; AC2456.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Complete proteome.
SQ SEQUENCE 347 AA; 40541 MW; AFBC249221FEB26D CRC64;

Query Match 49.0%; Score 49; DB 2; Length 347;
Best Local Similarity 52.6%; Pred. No. 12;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 LVVPAIKKDYGSQEDFTQV 20
   |.|  |||  |||  |||  |||
Db 329 LEUPIIKKEISSVKEFTQV 347

RESULT 7
Q8YLU3 PRELIMINARY; PRT; 347 AA.
AC Q8YLU3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alr5203 protein.
GN OrderedLocusNames=alr5203;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OC NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003599; BAB76902.1; -.
DR PIR; AC2456; AC2456.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Complete proteome.
SQ SEQUENCE 347 AA; 40541 MW; AFBC249221FEB26D CRC64;

Query Match 49.0%; Score 49; DB 2; Length 347;
Best Local Similarity 52.6%; Pred. No. 12;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 LVVPAIKKDYGSQEDFTQV 20
   |.|  |||  |||  |||  |||
Db 329 LEUPIIKKEISSVKEFTQV 347

RESULT 7
Q8YLU3 PRELIMINARY; PRT; 347 AA.
AC Q8YLU3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alr5203 protein.
GN OrderedLocusNames=alr5203;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OC NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003599; BAB76902.1; -.
DR PIR; AC2456; AC2456.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Complete proteome.
SQ SEQUENCE 347 AA; 40541 MW; AFBC249221FEB26D CRC64;
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Q9KUB9 PRELIMINARY; PRT; 764 AA.
AC Q9KUB9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VC0603.
GN OrderedLocusNames=VC0603;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OC NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406933; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004145; RAF93770.1; -.
DR PIR; B82303; B82303.
DR TIGR; VC0603; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 764 AA; 85616 MW; 0C3CC8BCA100C840 CRC64;

Query Match 49.0%; Score 49; DB 2; Length 764;
Best Local Similarity 45.0%; Pred. No. 29;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 LLVVPAPKDYGSQEDFTQV 20
   :|||  |||  |||  |||  |||
Db 235 IIIAVDIDSTDKSQEDFTNL 254

RESULT 8
Q9P919 PRELIMINARY; PRT; 173 AA.
AC Q9P919;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Manganese-dependent superoxide dismutase (EC 1.15.1.1)
DE (Fragment).
DE Name=soda;
GN Pneumocystis carinii f. sp. suis.
OS Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OC NCBI_TaxID=112251;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20427437; PubMed=10975697;
RA Denis C.M., Mazars E., Guyot K., Odberg-Ferragut C., Viscogliosi E.,
RA Dei-Cas E., Wakefield A.B.;
RT "Genetic divergence at the SODA locus of six different formae
RT speciales of Pneumocystis carinii.";
RL Med. Mycol. 38:289-300(2000).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
```

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CC family.
DR EMBL; AF146755; AAF25727.1; -.
DR HSP; O92450; 1KKC.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF02777; Sod Fe C; 1.
DR Pfam; PF00081; Sod_Fe_N; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR PRODOM; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 173
SQ SEQUENCE 173 AA; 20099 MW; 69110BFD0005665B CRC64;

Query Match 48.0%; Score 48; DB 2; Length 173;
Best Local Similarity 50.0%; Pred. No. 8.3;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 VVPAIKKDYGSQEDFTQV 20
Db 85 LVFAIKKDWGVENFISI 102

RESULT 9
Q66GG7 PRELIMINARY; PRT; 89 AA.
ID Q66GG7
AC Q66GG7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=IPTB0015;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenail-Francoise V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the genome evolution of Yersinia pseudotuberculosis,"
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAH19255.1; -.
DR InterPro; IPR009383; DUF1040.
DR Pfam; PF06288; DUF1040; 1.
KW Hypothetical protein.
SQ SEQUENCE 89 AA; 10168 MW; C240C03A620D66F9 CRC64;

Query Match 47.0%; Score 47; DB 2; Length 89;
Best Local Similarity 60.0%; Pred. No. 5.8;
Matches 9; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 3 VVPAIKKDYGSQEDF 17
Db 64 VIPGLKKDY--EEDF 76

RESULT 10
Q9RB12 PRELIMINARY; PRT; 89 AA.
ID Q9RB12
AC Q9RB12;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE YihD.
GN Name=yihD;
OS Pectobacterium carotovorum (subsp. carotovorum) (Erwinia carotovora
(subsp. carotovora)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=555;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI193;
RX MEDLINE=99392457; PubMed=10463161;
RA Vincent-Sealy L.V., Thomas J.D., Commander P., Salmoud G.P.;
RT "Erwinia carotovora DsbA mutants: evidence for a periplasmic-stress
signal transduction system affecting transcription of genes encoding
secreted proteins,";
RL Microbiology 145:1945-1958(1999).
DR EMBL; AF146615; AAD47615.1; -.
DR InterPro; IPR009383; DUF1040.
DR Pfam; PF06288; DUF1040; 1.
SQ SEQUENCE 89 AA; 10402 MW; 228FDDDD71E865481 CRC64;

Query Match 47.0%; Score 47; DB 2; Length 89;
Best Local Similarity 60.0%; Pred. No. 5.8;
Matches 9; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 3 VVPAIKKDYGSQEDF 17
Db 64 VIPGLKKDY--EEDF 76

RESULT 11
Q8ZJS3 PRELIMINARY; PRT; 89 AA.
ID Q8ZJS3
AC Q8ZJS3; Q74YD0; Q7CG24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein YPO0013a (Hypothetical protein y3814).
GN Name=YPO0013a; OrderedLocusNames=YPO015, y3814;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague,";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
DOI=10.1126/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM,";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
```

[illegible]

GN Name=cro;
 OS Lactococcus bacteriophage phi31.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=46654;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21141825; PubMed=11229902;
 RX DOI=10.1128/AEM.67.3.1128-1139.2001;
 RA Madsen S.M., Mills D., Djordjevic G., Israelsen H., Klaenhammer T.R.;
 RT "Analysis of the genetic switch and replication region of a P335-type
 RT bacteriophage with an obligate lytic lifestyle on Lactococcus
 RT lactis.";
 RL Appl. Environ. Microbiol. 67:1128-1139(2001).
 DR EMBL; AJ292531; CAC04155.1; -
 DR InterPro; IPR008003; DUF739.
 DR InterPro; IPR010982; Lambda_like_DNA.
 DR Pfam; PF05339; DUF739; 1.
 SQ SEQUENCE 74 AA; 8533 MW; B42A2F18180B5867 CRC64;

Query Match 46.0%; Score 46; DB 2; Length 74;
 Best Local Similarity 61.5%; Pred. No. 7.1;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 IKKDYGSQEDFTQ 19
 ||:|||||:
 Db 12 IKKDYGSQDFAK 24

Search completed: February 5, 2005, 20:04:40
 Job time : 97.9153 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:34:18 ; Search time 99.5085 Seconds
(without alignments)
73.847 Million cell updates/sec

Title: US-09-780-669-114_COPY_151_169

Perfect score: 106

Sequence: 1 GFTNYTDFEDSPYFKENSA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 396760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	19	4	AAM01157 Human pro
2	106	100.0	19	4	AAU69802 Human pro
3	106	100.0	19	4	AAG99042 Human pro
4	106	100.0	19	4	ABU71693 Prostate
5	106	100.0	19	5	ABB95262 Epitope m
6	106	100.0	19	6	ABR54374 Prostate
7	106	100.0	19	7	ADB13954 Human pro
8	106	100.0	19	7	ADG26370 Human pro
9	106	100.0	172	7	ADD69590 Human REM
10	106	100.0	174	8	ADP81123 Protein o
11	106	100.0	214	8	ADR65994 Human pro
12	106	100.0	214	8	ADR66892 Human pro
13	106	100.0	233	6	AAW75060 Human sec
14	106	100.0	233	6	ABO01936 Novel hum
15	106	100.0	240	4	ASG62153 Human P50
16	106	100.0	240	5	ABB89113 Human pol
17	106	100.0	241	2	AAW69386 Prostate
18	106	100.0	241	2	AAW59954 Amino aci
19	106	100.0	241	2	AAW71870 Human aci
20	106	100.0	241	2	AAW58380 Human sec
21	106	100.0	241	3	AAW82003 Human imm
22	106	100.0	241	3	ABG94412 Human pro
23	106	100.0	241	3	ABG94412 Human pro
24	106	100.0	241	4	AAU69764 Human pro
25	106	100.0	241	4	AAW74801 Prostate

ALIGNMENTS

RESULT 1

AAM01157
ID AAM01157 standard; peptide; 19 AA.

XX AAM01157;

DT 04-OCT-2001 (first entry)

XX Human prostate-specific peptide used in epitope mapping studies #14.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;

KW cytostatic; gene therapy; metastasis.

XX Homo sapiens.

XX WO200151633-A2.

XX 19-JUL-2001.

XX 16-JAN-2001; 2001WO-US001574.

XX 14-JAN-2000; 2000US-00483672.

XX (CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;

XX WPI; 2001-425873/45.

PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.

XX Claim 2; Page 399; 543pp; English.

CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate

AAG99003 Human pro
ABU71654 Prostate
ABU90579 Human AR4
AAU04962 Human pro
ABG96434 Human ova
ABG95223 Human N1-
ABG76666 Prostate
ABR54335 Prostate
ABR75601 Prostate
ADB13564 Human pro
ADG25980 Human pro
ADN39286 Cancer/an
ABG96433 Human ova
ADB75599 Prostate
AAW61618 Clone HPW
ABW01500 Human rec
AAY36171 Human sec
AAY36218 Human sec
ADJ45976 Novel hum
ADJ46070 Novel hum

26 106 100.0 241 4 AAG99003
27 106 100.0 241 4 ABU71654
28 106 100.0 241 4 ABU90579
29 106 100.0 241 4 AAU04962
30 106 100.0 241 5 ABG96434
31 106 100.0 241 5 ABG95223
32 106 100.0 241 5 ABG76666
33 106 100.0 241 6 ABR54335
34 106 100.0 241 6 ABR75601
35 106 100.0 241 7 ADB13564
36 106 100.0 241 7 ADG25980
37 106 100.0 241 7 ADN39286
38 106 100.0 258 5 ABG96433
39 106 100.0 258 7 ADB75599
40 106 100.0 273 2 AAW61618
41 106 100.0 273 7 ABW01500
42 87 82.1 43 2 AAY36171
43 87 82.1 43 2 AAY36218
44 87 82.1 43 7 ADJ45976
45 87 82.1 43 7 ADJ46070

CC	antigenic epitopes or domains of prostate specific proteins
XX	
SS	Sequence 19 AA;
QQ	Query Match 100.0%; Score 106; DB 4; Length 19; Best Local Similarity 100.0%; Pred. No. 6.2e-09; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GFNTNYTDFEDSPYFKENSA 19 1 GFNTNYTDFEDSPYFKENSA 19
Dd	
DD	RESULT 3 AAG99042
ID	AAG99042 standard; peptide; 19 AA.
XX	
AC	AAG99042;
XX	
DT	25-SEP-2001 (first entry)
DE	Human prostate-specific epitope mapping peptide #14.
KW	Human; prostate cancer; therapy; diagnosis; cat eye syndrome; chromosome 22q11.2; prostate-specific protein; chromosome 1; prostate specific antigen; PSA.
KW	
KX	Homo sapiens.
OS	WO200134802-A2.
XX	
PN	17-MAY-2001.
PD	
XX	09-NOV-2000; 2000MO-USO30904.
PF	
XX	12-NOV-1999; 99US-00439313.
PR	18-NOV-1999; 99US-00443686.
XX	(CORI-) CORIXA CORP.
PA	
XX	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG; Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A; WPI; 2001-308785/32.
DR	
XX	Isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, useful in the diagnosis and therapy of prostate cancer.
PT	
PT	
XX	Claim 3; Page 299; 325pp; English.
XX	The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P774P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) p501S was located on chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification of the present invention
CC	
CC	Sequence 19 AA;
XX	
XX	Query Match 100.0%; Score 106; DB 4; Length 19; Best Local Similarity 100.0%; Pred. No. 6.2e-09; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 GFNTNYTDFEDSPYFKENSA 19 1 GFNTNYTDFEDSPYFKENSA 19
Dd	

CC prostate cancer therapy associated peptide. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?DocID=US20020192763

XX ABU71693 standard; peptide; 19 AA.

AC ABU71693;

XX 10-JUN-2003 (first entry)

XX Prostate cancer therapy associated peptide #15.

XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KW PSMA.

XX Homo sapiens.

XX US2002192763-A1.

XX 19-DEC-2002.

XX 29-JUN-2001; 2001US-00895793.

XX 04-OCT-1999; 99US-0157455P.

XX 04-OCT-2000; 2000US-00679272.

XX 28-MAR-2001; 2001US-00822827.

XX (XUJJ/) XU J.

XX (DILL/) DILLON D C.

XX (MITC/) MITCHAM J L.

XX (HARL/) HARLOCKER S L.

XX (JIAN/) JIANG Y.

XX (KALO/) KALOS M D.

XX (FANG/) FANGER G R.

XX (RETT/) RETTER M W.

XX (STOL/) STOLK J A.

XX (DAYC/) DAY C H.

XX (VEDV/) VEDVICK T S.

XX (CART/) CARTER D.

XX (LISX/) LI S X.

XX (WANG/) WANG A.

XX (SKEI/) SKEIKY Y A W.

XX (HEPL/) HEPLER W T.

XX (HEND/) HENDERSON R A.

XX (HURA/) HURAL J.

XX (MCNE/) MCNEILL P D.

XX (HOUG/) HOUGHTON R L.

XX (DBAS/) Y DE BASSOLS C V.

XX (FOYT/) FOY T M.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
 PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
 XX WPI; 2001-245062/25.

XX Prostate specific protein and its encoding polynucleotide, useful for the
 PT treatment and diagnosis of prostate cancer.

XX Example 18; SEQ ID NO 504; 85pp; English.

XX The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 35 sequences defined in the USPTO web
 CC site, which is encoded by any of the 4 nucleotide sequences not defined
 CC in the specification. The fusion protein, composition and methods are
 CC useful for diagnosing, preventing and/or treating cancer, particularly
 CC prostate cancer. The proteins are useful as markers to indicate the
 CC presence or absence of cancer. This is the amino acid sequence of a

SQ Sequence 19 AA;

Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYPKNSA 19
 |||||
 Db 1 GFTNYTDFEDSPYPKNSA 19

RESULT 5

ABB95262

ID ABB95262 standard; peptide; 19 AA.

XX AC ABB95262;

XX 19-JUL-2002 (first entry)

XX Epitope mapping study peptide SEQ ID NO 504.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
 KW gene therapy.

XX Unidentified.

XX US2002022248-A1.

XX 21-FEB-2002.

XX 12-JAN-2001; 2001US-00759143.

XX 25-FEB-1997; 97US-00806099.

XX 01-AUG-1997; 97US-00904804.

XX 10-FEB-1998; 98US-00020956.

XX 25-FEB-1998; 98US-00030607.

XX 14-JUL-1998; 98US-00115453.

XX 23-SEP-1998; 98US-00159812.

XX 15-JAN-1999; 99US-00232149.

XX 09-APR-1999; 99US-00288946.

XX 13-JUL-1999; 99US-00352616.

XX 12-NOV-1999; 99US-00439313.

XX 18-NOV-1999; 99US-00443686.

XX 14-JAN-2000; 2000US-00483672.

XX 27-MAR-2000; 2000US-00536857.

XX 12-MAY-2000; 2000US-00568100.

XX 13-JUN-2000; 2000US-00570737.

XX 27-JUN-2000; 2000US-00605783.

XX 10-AUG-2000; 2000US-00636215.

XX 29-AUG-2000; 2000US-00651236.

XX 06-SEP-2000; 2000US-00657279.

XX 02-OCT-2000; 2000US-00679426.

XX 10-OCT-2000; 2000US-00685166.

XX (XUJJ/) XU J.

XX (DILL/) DILLON D C.

XX (MITC/) MITCHAM J L.

XX (HARL/) HARLOCKER S L.

XX (JIAN/) JIANG Y.

XX (KALO/) KALOS M D.

XX (FANG/) FANGER G R.

XX (RETT/) RETTER M W.

XX (STOL/) STOLK J A.

XX (DAYC/) DAY C H.

XX (VEDV/) VEDVICK T S.

XX (CART/) CARTER D.

XX (LISX/) LI S X.

PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
XX
PS Claim 2; SEQ ID NO 504; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a
CC peptide described in the invention
XX
XX Sequence 19 AA;
SQ
Query Match 100.0%; Score 106; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19
RESULT 6
ABR54374
ID ABR54374 standard; protein; 19 AA.
XX
AC ABR54374;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostate tumour specific related peptide for epitope mapping SEQ ID 504.
XX
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
XX immune response; prostate cancer.
XX
XX Homo sapiens.
XX
XX WO200289747-A2.
XX
XX 14-NOV-2002.
XX
XX 09-MAY-2002; 2002WO-US014753.
XX
XX 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00895814.
XX 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
XX Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
XX Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
XX McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
XX Deng T;
XX
XX WPI; 2003-167130/16.
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
XX

PS Example 18; Page 466; 691pp; English.
XX
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
XX Sequence 19 AA;
SQ
Query Match 100.0%; Score 106; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19
RESULT 7
ADB13954
ID ADB13954 standard; peptide; 19 AA.
XX
AC ADB13954;
XX
DT 18-DEC-2003 (first entry)
XX
XX Human prostate protein P503S epitope mapping peptide #2101.
XX
XX Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
KW cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell; epitope.
XX
XX Homo sapiens.
XX
XX US2003185830-A1.
XX
XX 02-OCT-2003.
XX
XX 12-NOV-2002; 2002US-00294025.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 23-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00433913.
XX 18-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.
XX 09-FEB-2001; 2001US-00780669.
XX 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00895814.
XX 10-DEC-2001; 2001US-00012896.
XX 09-MAY-2002; 2002US-00144678.
XX

PA (CORI-) CORIXA CORP.
XX Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
XX New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX Example 18; Page; 101pp; English.
XX The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC peptides comprise a fragment ADB13563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADB1358, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is an epitope or
CC peptide derived from one of the prostate specific proteins of the
CC invention. Note: Except where otherwise indicated, the sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030185830.
XX
SQ Sequence 19 AA;
Query Match 100.0%; Score 106; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. NO. 6.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19
RESULT 8
ADG26370
ID ADG26370 standard; peptide; 19 AA.
XX AC ADG26370;
XX 26-FEB-2004 (first entry)
XX Human prostate-specific polypeptide #43.
XX Human; prostate-specific polypeptide; prostate cancer; cytostatic.
XX Homo sapiens.

XX US2003157089-A1.
XX 21-AUG-2003.
XX 09-MAY-2002; 2002US-00144678.
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.
XX 09-FEB-2001; 2001US-00780669.
XX 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00895814.
XX 10-DEC-2001; 2001US-00012896.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
XX Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
XX Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
XX McNeill PD, Houghton RL, Vinals Y De Bassolec, Foy TW, Watanabe Y;
XX Mesgher MJ, Deng T;
XX WPI; 2003-777973/73.
XX New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX Example 18; SEQ ID NO 504; 99pp; English.
XX The invention relates to human prostate-specific polypeptides and the
CC polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents a human prostate-specific polypeptide of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 19 AA;
Query Match 100.0%; Score 106; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. NO. 6.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFTNYTDFEDSPYFKENSA 19

DB 1 GFTNYTDFEDSPYFKENSA 19
|||||

RESULT 9
ADD69590
ID ADD69590 standard; protein; 172 AA.
XX
AC ADD69590;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human REMAP protein - SEQ ID 19.
XX
KW human; receptor and membrane-associated protein; REMAP; cytostatic;
KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
KW thymomimetic; cell proliferative; cancer; atherosclerosis; neurological;
KW epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS;
KW allergy; developmental; hypothyroidism; Cushing's syndrome; infection.
XX
OS Homo sapiens.
XX
PN WO2003048305-A2.
XX
PD 12-JUN-2003.
XX
PF 13-NOV-2002; 2002WO-US036759.
XX
PR 13-NOV-2001; 2001US-0333097P.
PR 15-NOV-2001; 2001US-0335274P.
PR 14-DEC-2001; 2001US-0340542P.
PR 18-DEC-2001; 2001US-0342166P.
PR 11-JAN-2002; 2002US-0347580P.
PR 14-JAN-2002; 2002US-0348687P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Duggan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y;
PI Chawla NK, Warren BA, Barroso I, Becha SD, Yue H, Lehn-Mason PM;
PI Thangavelu K, Lee S, Emmerling BM, Kable AE, Khare R, Baughn MR;
PI Gandhi AR, Tran UK, Richardson TW, Marquis JP, Lal PG, Forsythe IJ;
PI Lee EA, Swarnakar A, Kallio DA, Griffin JA, Elliott VS, Gorvad AE;
PI Hafalia AJA, Ison CH, Jin P, Jiang X, Jackson AA, Bhatia U;
PI Burdill JD, Blake JJ, Ho A, Zheng W, Gao J;
XX
DR WPI; 2003-513744/48.
DR N-PSDB; ADD69637.
XX
PT New human receptors and membrane-associated proteins (REMAP), useful for
PT diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or
PT infections.
XX
PS Claim 1; SEQ ID NO 19; 298pp; English.
XX
CC The invention relates to a novel isolated polypeptide comprising a human
CC receptor and membrane-associated protein (REMAP). The polypeptide of the
CC invention demonstrates cytostatic, antiarteriosclerotic, anticonvulsant,
CC nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
CC antiinflammatory and thymomimetic activities and may be useful for
CC treating and diagnosing various disorders including those which are cell
CC proliferative such as cancer and atherosclerosis, neurological including
CC epilepsy, Huntington's disease and stroke, immune/inflammatory
CC particularly AIDS and allergies and developmental such as hypothyroidism
CC and Cushing's syndrome, as well as infections. The current sequence is
CC that of the human REMAP protein of the invention.
XX
SQ Sequence 172 AA;
Query Match 100.0%; Score 106; DB 7; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
|||||

DB 82 GFTNYTDFEDSPYFKENSA 100
|||||

RESULT 10
ADP81123
ID ADP81123 standard; protein; 174 AA.
XX
AC ADP81123;
XX
DT 09-SEP-2004 (first entry)
XX
DE Protein of human ovarian specific gene, SEQ ID NO 157.
XX
KW normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;
KW metastatic; cancer; vaccine; cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO2004053079-A2.
XX
PD 24-JUN-2004.
XX
PF 08-DEC-2003; 2003WO-US038855.
XX
PR 06-DEC-2002; 2002US-0431301P.
PR 30-JUN-2003; 2002US-0431321P.
PR 07-NOV-2003; 2003US-0518607P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Turner LR, Sun Y, Liu S, Chen H;
XX
DR WPI; 2004-468850/44.
DR N-PSDB; ADP80988.
XX
PT New ovarian specific nucleic acid molecules and polypeptides useful for
PT diagnosing, preventing or treating ovarian cancer, for producing
PT transgenic animals or cells, or for research purposes.
XX
PS Claim 12; SEQ ID NO 157; 754pp; English.
XX
CC The invention relates to novel isolated nucleic acid molecules and
CC polypeptides present in normal and neoplastic ovarian cells. These
CC comprise a nucleic acid sequence encoding any of the 167 amino acid
CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
CC specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
CC in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
CC further comprises a method for determining the presence of a ovarian
CC specific nucleic acid (OSNA) in a sample; a vector comprising the above
CC nucleic acid molecule; a host cell comprising the vector; a method for
CC producing a polypeptide encoded by the above nucleic acid molecule; a
CC or its fragment that specifically binds to the above polypeptide; a
CC method for determining the presence of an ovarian specific protein in a
CC sample; a method for diagnosing or monitoring the presence and metastases
CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or
CC presence of cancer in a patient; the kit comprising a means for
CC determining the presence of the above nucleic acid molecule or
CC polypeptide; a method of treating a patient with ovarian cancer; and a
CC vaccine comprising the above polypeptide or nucleic acid encoding the
CC polypeptide. The isolated nucleic acid molecules and polypeptides have
CC cytostatic activity. The isolated polypeptides may be used to create a
CC vaccine. The isolated nucleic acid molecules and polypeptides can be used
CC for diagnosing or monitoring the presence and metastases of ovarian
CC cancer and treating ovarian cancer. This sequence represents the protein
CC of an ovarian specific gene of the invention.
XX
SQ Sequence 174 AA;

Query Match 100.0%; Score 106; DB 8; Length 174;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
|||||
DB 39 GFTNYTDFEDSPYFKENSA 57

RESULT 11
ADR65994
ID ADR65994 standard; protein; 214 AA.

XX AC ADR65994;
XX DT 02-DEC-2004 (first entry)
XX DE Human prostatic carcinoma derived protein SEQ ID 190 #1.
XX KW human; cytostatic; diagnosis; prostatic cancer;
XX KW differential expression analysis.

XX OS Homo sapiens.

XX PN WO2004076614-A2.

XX PD 10-SEP-2004.

XX PF 22-FEB-2004; 2004WO-DE000433.

XX PR 27-FEB-2003; 2003DE-01009985.

XX PR 14-MAY-2003; 2003DE-01022134.

XX PA (HINZ/) HINZMANN B.

XX PA (DAHL/) DAHL E.

XX PA (ROSE/) ROSENTHAL A.

XX PA (HERM/) HERMANN K.

XX PA (PILA/) PILARSKY C.

XX PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;
XX PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
XX PI Xinzhang L, Staub E;

XX DR WPI; 2004-653386/63.

XX PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
XX PT useful for diagnosis, treatment and in screening for specific binding
XX PT agents.

XX PS Claim 2; Page 585; 1607pp; German.

XX CC This invention describes novel cytostatic polynucleotide and polypeptide
XX CC sequences which can be used in a method for diagnosing prostatic cancer
XX CC or the risk of developing prostatic cancer. Diagnosis is based on
XX CC determining over transcription or over expression of the sequences in
XX CC prostatic tissue. Screening for inhibitors of the sequences or detection
XX CC substances involves a binding assay, any compounds that bind are
XX CC selected, optionally after deconvolution of mixtures. Detection of a
XX CC predetermined minimum level of the reporter indicates the presence of
XX CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
XX CC short-interfering RNA or ribozymes; an organic molecule of molecular
XX CC weight below 5000, preferably 300, that binds to the polypeptide; an
XX CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
XX CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
XX CC (monoclonal) antibody directed against Ab or any of the above derivatised
XX CC with a reporter group, cell toxin, immunostimulatory molecules and/or
XX CC radioisotope. The polynucleotides are identified in human prostatic
XX CC cancer by differential expression analysis, using DNA microarrays,
XX CC between normal and tumorous tissues, with (over)expression being detected
XX CC by quantitative PCR. Analysis of prostatic cancer samples showed that
XX CC CD24 was upregulated in many of them. Sections of tissue, isolated from
XX CC prostatic cancer patients, or subjects at risk, were incubated

CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65905-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.

XX SQ Sequence 214 AA;

Query Match 100.0%; Score 106; DB 8; Length 214;

Best Local Similarity 100.0%; Pred. No. 8.5e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19

|||||

DB 124 GFTNYTDFEDSPYFKENSA 142

RESULT 12

ADR66892
ID ADR66892 standard; protein; 214 AA.

XX AC ADR66892;

XX DT 02-DEC-2004 (first entry)

XX DE Human prostatic carcinoma derived DNA SEQ ID 190 #4.

XX KW human; cytostatic; diagnosis; prostatic cancer;
XX KW differential expression analysis.

XX OS Homo sapiens.

XX PN WO2004076614-A2.

XX PD 10-SEP-2004.

XX PF 22-FEB-2004; 2004WO-DE000433.

XX PR 27-FEB-2003; 2003DE-01009985.

XX PR 14-MAY-2003; 2003DE-01022134.

XX PA (HINZ/) HINZMANN B.

XX PA (DAHL/) DAHL E.

XX PA (ROSE/) ROSENTHAL A.

XX PA (HERM/) HERMANN K.

XX PA (PILA/) PILARSKY C.

XX PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;
XX PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
XX PI Xinzhang L, Staub E;

XX DR WPI; 2004-653386/63.

XX PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
XX PT useful for diagnosis, treatment and in screening for specific binding
XX PT agents.

XX PS Claim 2; Page 1545; 1607pp; German.

XX CC This invention describes novel cytostatic polynucleotide and polypeptide
XX CC sequences which can be used in a method for diagnosing prostatic cancer
XX CC or the risk of developing prostatic cancer. Diagnosis is based on
XX CC determining over transcription or over expression of the sequences in
XX CC prostatic tissue. Screening for inhibitors of the sequences or detection
XX CC substances involves a binding assay, any compounds that bind are
XX CC selected, optionally after deconvolution of mixtures. Detection of a
XX CC predetermined minimum level of the reporter indicates the presence of
XX CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
XX CC short-interfering RNA or ribozymes; an organic molecule of molecular

weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotypic, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, and normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR5805-ADR6954 represent the polynucleotide and polypeptide sequences used in the method of the invention.

Sequence 214 AA;

Query Match 100.0%; Score 106; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 8.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
Db 124 GFTNYTDFEDSPYFKENSA 142

RESULT 13

AAW75060
ID AAW75060 standard; protein; 233 AA.

XX AC AAW75060;

XX 25-MAR-2003 (revised)
DT 28-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 4 clone HKCSR70.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; fetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX Key Location/Qualifiers
FH Misc-difference 233
FT /label= unknown

XX WO9839446-A2.

XX 11-SEP-1998.

XX 06-MAR-1998; 98WO-US004482.

XX 07-MAR-1997; 97US-0038621P.

XX 07-MAR-1997; 97US-0040161P.

XX 07-MAR-1997; 97US-0040162P.

XX 07-MAR-1997; 97US-0040163P.

XX 07-MAR-1997; 97US-0040333P.

XX 07-MAR-1997; 97US-0040334P.

XX 07-MAR-1997; 97US-0040336P.

XX 11-APR-1997; 97US-0043311P.

PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047452P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056633P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.

PR 22-AUG-1997; 97US-0056889P.
 PR 22-AUG-1997; 97US-0056892P.
 PR 22-AUG-1997; 97US-0056893P.
 PR 22-AUG-1997; 97US-0056894P.
 PR 22-AUG-1997; 97US-0056903P.
 PR 22-AUG-1997; 97US-0056908P.
 PR 22-AUG-1997; 97US-0056909P.
 PR 22-AUG-1997; 97US-0056910P.
 PR 22-AUG-1997; 97US-0056911P.
 PR 05-SEP-1997; 97US-0057650P.
 PR 05-SEP-1997; 97US-0057661P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
 PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
 PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
 XX
 DR WPI; 1998-609887/51.
 DR N-PSDB; AAV34157.
 XX
 XX New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX
 PS Claim 1; Page 281-282; 447pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin FC
 CC portion (e.g. AAV34145) for increasing the stability of the fused protein
 CC as compared to the human protein only. The invention relates to 70 novel
 CC genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino
 CC acid sequences AAW75057-W75179) which are useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
 CC pathological conditions can be diagnosed by determining the amount of the
 CC new polypeptides in a sample or by determining the presence of mutations
 CC in the new polynucleotides. Specific uses are described for each of the
 CC 70 polynucleotides, based on which tissues they are most highly expressed
 CC in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
 CC PF field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 233 AA;

Query Match 100.0%; Score 106; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 9.3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
 |||||
 Db 142 GFTNYTDFEDSPYFKENSA 160

RESULT 14
 ABO01936
 ID ABO01936 standard; protein; 233 AA.
 XX
 AC ABO01936;
 XX
 DT 12-AUG-2003 (first entry)
 XX
 DE Novel human secreted protein #4.
 XX
 KW Human; immunoglobulin G; IgG; fragment of crystallisation; Fc;
 KW immune system disorder; haematopoietic cell disorder;
 KW immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
 KW Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
 KW blood coagulation disorder; blood platelet disorder; autoimmune disorder;
 KW Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
 KW glomerulonephritis; Grave's disease; allergic reaction;
 KW graft-versus-host disease; hyperproliferative disorder; neoplasm;
 KW infectious disease; nervous system disease; spinal cord disorder;

KW head trauma; stroke; tissue regeneration; congenital defect; trauma;
 KW wound; burn; incision; ulcer; age disease; osteoporosis;
 KW periodontal disease; liver failure; catabolism; anabolism; metabolism;
 KW food additive; preservative; secreted protein.

XX Homo sapiens.

OS US2003027132-A1.

XX 06-FEB-2003.

XX 04-SEP-1998; 98US-00148545.

XX 07-MAR-1997; 97US-0038621P.

XX 07-MAR-1997; 97US-0040161P.

XX 07-MAR-1997; 97US-0040162P.

XX 07-MAR-1997; 97US-0040163P.

XX 07-MAR-1997; 97US-0040333P.

XX 07-MAR-1997; 97US-0040334P.

XX 07-MAR-1997; 97US-0040336P.

XX 11-APR-1997; 97US-0043311P.

XX 11-APR-1997; 97US-0043312P.

XX 11-APR-1997; 97US-0043313P.

XX 11-APR-1997; 97US-0043314P.

XX 11-APR-1997; 97US-0043315P.

XX 11-APR-1997; 97US-0043568P.

XX 11-APR-1997; 97US-0043569P.

XX 11-APR-1997; 97US-0043570P.

XX 11-APR-1997; 97US-0043671P.

XX 11-APR-1997; 97US-0043672P.

XX 11-APR-1997; 97US-0043674P.

XX 23-MAY-1997; 97US-0047492P.

XX 23-MAY-1997; 97US-0047500P.

XX 23-MAY-1997; 97US-0047501P.

XX 23-MAY-1997; 97US-0047502P.

XX 23-MAY-1997; 97US-0047503P.

XX 23-MAY-1997; 97US-0047581P.

XX 23-MAY-1997; 97US-0047582P.

XX 23-MAY-1997; 97US-0047583P.

XX 23-MAY-1997; 97US-0047584P.

XX 23-MAY-1997; 97US-0047585P.

XX 23-MAY-1997; 97US-0047586P.

XX 23-MAY-1997; 97US-0047587P.

XX 23-MAY-1997; 97US-0047588P.

XX 23-MAY-1997; 97US-0047589P.

XX 23-MAY-1997; 97US-0047590P.

XX 23-MAY-1997; 97US-0047592P.

XX 23-MAY-1997; 97US-0047593P.

XX 23-MAY-1997; 97US-0047594P.

XX 23-MAY-1997; 97US-0047595P.

XX 23-MAY-1997; 97US-0047596P.

XX 23-MAY-1997; 97US-0047597P.

XX 23-MAY-1997; 97US-0047598P.

XX 23-MAY-1997; 97US-0047599P.

XX 23-MAY-1997; 97US-0047600P.

XX 23-MAY-1997; 97US-0047601P.

XX 23-MAY-1997; 97US-0047612P.

XX 23-MAY-1997; 97US-0047613P.

XX 23-MAY-1997; 97US-0047614P.

XX 23-MAY-1997; 97US-0047615P.

XX 23-MAY-1997; 97US-0047617P.

XX 23-MAY-1997; 97US-0047618P.

XX 23-MAY-1997; 97US-0047632P.

XX 23-MAY-1997; 97US-0047633P.

XX 06-JUN-1997; 97US-0048964P.

XX 06-JUN-1997; 97US-0048974P.

XX 22-AUG-1997; 97US-0056630P.

XX 22-AUG-1997; 97US-0056631P.

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PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057761P.
PR 06-MAR-1998; 98WO-US004482.
XX
FA (RUBE/) RUBEN S M.
FA (ROSE/) ROSEN C A.
FA (FISC/) FISCHER C L.
FA (SOPP/) SOPPET D R.
FA (CART/) CARTER K C.
FA (BEDN/) BEDNARIK D R.
FA (ENDR/) ENDRESS G A.
FA (YUGG/) YU G.
FA (NIJJ/) NI J.
FA (FENG/) FENG P.
FA (YOUN/) YOUNG P E.
FA (GREE/) GREENE J M.
FA (FERR/) FERRIE A M.
FA (DUAN/) DUAN R.
FA (HUJJ/) HU J.
FA (FLOR/) FLORENCE K A.
FA (OLSE/) OLSEN H S.
FA (EBNE/) EBNER R.
FA (BREW/) BREWER L A.
FA (SHIY/) SHI Y.
XX
PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Shi Y;
XX
DR WPI: 2003-466138/44.
DR N-PSDB; ACD08028.
XX
PT Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing
PT or treating deficiencies or disorders of the immune system, autoimmune
PT disorders, hyperproliferative disorders, and infectious diseases.
XX
PS Claim 11; Page 173; 243pp; English.
XX
CC The invention describes an isolated human secreted HODAZ50 polypeptide
CC (I) comprising a sequence at least 95% identical to a sequence selected
CC from polypeptide fragment of any one of the 123 polypeptide sequences

CC (PS) fully defined in the specification and having biological activity,
CC polypeptide domain or epitope of PS, secreted form of PS, full-length
CC protein of PS, or variant, allelic variant or species homologues of PS.
CC (I) or a polynucleotide (II) encoding (I) is useful for preventing,
CC treating, or ameliorating a medical condition in a mammalian subject. (I)
CC or (II) is also useful for diagnosing a pathological condition or a
CC susceptibility to a pathological condition in a subject. (I) is useful
CC for identifying a binding partner which involves contacting the
CC polypeptide with the binding partner and determining whether the binding
CC partner affects the activity of the polypeptide. (I) or (II) is useful
CC for diagnosing or treating deficiencies or disorders of the immune
CC system, deficiencies or disorders of haematopoietic cells, to treat
CC immunologic deficiency disorders, ataxia telangiectasia, HIV infection,
CC Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood
CC coagulation disorders, blood platelet disorders, autoimmune disorders
CC (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis,
CC dermatitis, glomerulonephritis, Grave's disease), allergic reactions,
CC graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms,
CC located in the abdomen, bone, breast, digestive system, liver, pancreas,
CC peritoneum, endocrine glands), infectious diseases (e.g., viral,
CC bacterial, fungal or parasitic infection), central and peripheral nervous
CC system diseases (e.g., spinal cord disorders, head trauma or stroke), to
CC differentiate, proliferate and attract cells leading to the regeneration
CC of tissues to repair, replace or protect tissue damaged by congenital
CC defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g.,
CC osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV)
CC is useful to modulate mammalian characteristics, to modulate mammalian
CC metabolism affecting catabolism, anabolism, processing, utilisation, and
CC storage of energy, to change a mammal's mental state or physical state,
CC or as a food additive or preservative, such as to increase or decrease
CC storage capabilities, fat content, lipid, protein, carbohydrate,
CC vitamins, minerals, cofactors or other nutritional components. This is
CC the amino acid sequence of a novel human secreted protein

XX SQ Sequence 233 AA;

Query Match 100.0%; Score 106; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 9.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
Db 142 GFTNYTDFEDSPYFKENSA 160

RESULT 15
AAG62153
ID AAG62153 standard; protein; 240 AA.
XX
XX AAG62153;
XX
XX 06-JUL-2001 (first entry)
XX
XX Human P503S inventive antigen SEQ ID NO: 352.

XX Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;
XX chromosome 11p13; zinc finger transcription factor.

XX Homo sapiens.
XX WO200125273-A2.
XX
XX 12-APR-2001.
XX
XX 04-OCT-2000; 2000WO-US027465.
XX
XX 04-OCT-1999; 99US-0157459P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Xu J, Cheever MA, Reed SG;
XX WPI: 2001-328324/34.

XX Polypeptide comprising part of the Wilms Tumor gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with WT1.
XX
XX
PS Disclosure; Page 223-224; 228pp; English.
XX
CC The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein WT1 and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WT1
CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukaemia. The present sequence is
CC a polypeptide described in the exemplification of the invention
XX
SQ Sequence 240 AA;
Query Match 100.0%; Score 106; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFTNYTDFEDSPYKNSA 19
Db 151 GFTNYTDFEDSPYKNSA 169
Search completed: February 5, 2005, 19:59:55
Job time : 100.508 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	106	100.0	19	3	US-09-439-313-504	Sequence 504, App
2	106	100.0	19	4	US-09-636-215-504	Sequence 504, App
3	106	100.0	19	4	US-09-685-168A-504	Sequence 504, App
4	106	100.0	19	4	US-09-679-426-504	Sequence 504, App
5	106	100.0	19	4	US-09-759-143-504	Sequence 504, App
6	106	100.0	19	4	US-09-651-236-504	Sequence 504, App
7	106	100.0	233	4	US-09-148-545-137	Sequence 137, App
8	106	100.0	241	3	US-08-808-148-1	Sequence 1, Appli
9	106	100.0	241	3	US-09-020-956-114	Sequence 114, App
10	106	100.0	241	3	US-09-030-607-114	Sequence 114, App
11	106	100.0	241	3	US-09-439-313-114	Sequence 114, App
12	106	100.0	241	3	US-09-352-616A-114	Sequence 114, App
13	106	100.0	241	4	US-09-232-149A-114	Sequence 114, App
14	106	100.0	241	4	US-09-159-812-114	Sequence 114, App
15	106	100.0	241	4	US-09-636-215-114	Sequence 114, App
16	106	100.0	241	4	US-09-685-166A-114	Sequence 114, App
17	106	100.0	241	4	US-09-115-453-114	Sequence 114, App
18	106	100.0	241	4	US-09-688-489-114	Sequence 114, App
19	106	100.0	241	4	US-09-679-426-114	Sequence 114, App
20	106	100.0	241	4	US-09-759-143-114	Sequence 114, App
21	106	100.0	241	4	US-09-651-236-114	Sequence 114, App
22	87	82.1	43	4	US-09-663-600A-129	Sequence 129, App
23	87	82.1	43	4	US-09-663-600A-223	Sequence 223, App
24	51	48.1	249	4	US-09-949-016-8334	Sequence 8334, Ap
25	49	46.2	252	3	US-08-705-771-17	Sequence 17, Appl
26	49	46.2	252	4	US-09-417-540-17	Sequence 17, Appl
27	45	42.5	223	4	US-09-270-767-61548	Sequence 61548, A

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; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-636-215-504

Query Match      100.0%; Score 106; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTNYTDFEDSPYFKENSA 19
Db      1 GFTNYTDFEDSPYFKENSA 19

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; Sequence 504, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-679-426-504

Query Match      100.0%; Score 106; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTNYTDFEDSPYFKENSA 19
Db      1 GFTNYTDFEDSPYFKENSA 19

RESULT 5
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; Sequence 504, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick

```

APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 504
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-759-143-504

Query Match 100.0%; Score 106; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
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Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 6
US-09-651-236-504
Sequence 504, Application US/09651236
Patent No. 6818751
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 504
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-651-236-504

Query Match 100.0%; Score 106; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
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Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 7
US-09-148-545-137
Sequence 137, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
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EARLIER FILING DATE: 1998-03-06
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EARLIER APPLICATION NUMBER: 60/047,632
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EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23

Mon Feb 7 16:18:28 2005

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EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/047,595

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EARLIER APPLICATION NUMBER: 60/057,761
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EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,585
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EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,593
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EARLIER APPLICATION NUMBER: 60/047,614
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 137
LENGTH: 233

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Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 142 GFTNYTDFEDSPYFKENSA 160

RESULT 8
US-08-808-148-1
; Sequence 1, Application US/08808148
; Patent No. 6020478
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer


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; APPLICANT: Goli, Surya
; APPLICANT: Zhang, Hong Wolfe
; TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,148
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0218 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT26
; CLONE: 2187263
; US-08-808-148-1

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Query Match 100.0%; Score 106; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 151 GFTNYTDFEDSPYFKENSA 169

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RESULT 9
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; Sequence 114, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-020-956-114

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Query Match 100.0%; Score 106; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 151 GFTNYTDFEDSPYFKENSA 169

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RESULT 10
US-09-030-607-114
; Sequence 114, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun C.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-030-607-114

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; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-636-215-114

Query Match 100.0%; Score 106; DB 4; Length 241;
Best Local Similarity 100.0%; Pred.No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: February 5, 2005, 20:07:13
Job time : 25.1525 secs

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Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
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 Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 2

US-09-780-669-504
 ; Sequence 504, Application US/09780669
 ; Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqi
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 APPLICANT: Hural, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.427C24
 CURRENT APPLICATION NUMBER: US/09/780,669
 CURRENT FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 943
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 504

LENGTH: 19

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab

US-09-780-669-504

Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
 |||||
 Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 3

US-09-822-827-504
 ; Sequence 504, Application US/09822827
 ; Patent No. US20020081680A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.534C1
 CURRENT APPLICATION NUMBER: US/09/822,827
 CURRENT FILING DATE: 2001-03-28
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 504

LENGTH: 19
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab

US-09-822-827-504

Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
 |||||
 Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 4

US-09-895-793-504
 ; Sequence 504, Application US/09895793
 ; Publication No. US20020192763A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Harlocker, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqi
 APPLICANT: Kalos, Michael D.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William T.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Hural, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 APPLICANT: Vinals de Bassols, Carlota
 APPLICANT: Foy, Teresa
 APPLICANT: Fanger, Gary R.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.534C2
 CURRENT APPLICATION NUMBER: US/09/895,793
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 504
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Made in a lab

US-09-895-793-504

Query Match 100.0%; Score 106; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
 |||||
 Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 5

US-09-895-814-504
 ; Sequence 504, Application US/09895814
 ; Publication No. US20020193296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun

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; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-895-814-504

Query Match      100.0%; Score 106; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTNYTDFEDSPYFKNSA 19
Db      1 GFTNYTDFEDSPYFKNSA 19

RESULT 6
US-10-012-896-504
; Sequence 504, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
```

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; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-012-896-504

Query Match      100.0%; Score 106; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTNYTDFEDSPYFKNSA 19
Db      1 GFTNYTDFEDSPYFKNSA 19

RESULT 7
US-10-010-940-504
; Sequence 504, Application US/10010940
; Publication No. US2003008062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-010-940-504

Query Match      100.0%; Score 106; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTNYTDFEDSPYFKNSA 19
Db      1 GFTNYTDFEDSPYFKNSA 19

RESULT 8
US-10-144-678A-504
; Sequence 504, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
```

```

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-144-678A-504

Query Match 100.0%; Score 106; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 9
US-10-294-025-504
; Sequence 504, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-294-025-504

Query Match 100.0%; Score 106; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19

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Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 10
US-09-981-876-137
; Sequence 137, Application US/09981876
; Patent No. US20020184689A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
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; PRIOR APPLICATION NUMBER: 60/047,500
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; PRIOR APPLICATION NUMBER: 60/047,598
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; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632

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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
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; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,669
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,312
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; PRIOR APPLICATION NUMBER: 60/043,313
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,672
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; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,877
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,889
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,893
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
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; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22

; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 05-Sep-1997
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
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; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
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; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233

Query Match 100.0%; Score 106; DB 9; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
| | | | | | | | | | | | | | | | | | | | |
Db 142 GFTNYTDFEDSPYFKENSA 160

RESULT 11
US-09-148-545-137
; Sequence 137, Application US/09148545

```

; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
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; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
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; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/043,312
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; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,882
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599

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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
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EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
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EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 137
LENGTH: 233

Query Match 100.0%; Score 106; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 142 GFTNYTDFEDSPYFKENSA 160
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RESULT 12
US-10-264-237-1489
Sequence 1489, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1489
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-237-1489

Query Match 100.0%; Score 106; DB 15; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 150 GFTNYTDFEDSPYFKENSA 168
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RESULT 13
US-09-759-143-114
Sequence 114, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 114
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapien
US-09-759-143-114

Query Match 100.0%; Score 106; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 151 GFTNYTDFEDSPYFKENSA 169
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RESULT 14
US-09-780-669-114
Sequence 114, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.

```

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-780-669-114

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Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFTNYTDFEDSPYFKENSA 19
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Db      151 GFTNYTDFEDSPYFKENSA 169
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Db      151 GFTNYTDFEDSPYFKENSA 169
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RESULT 15
US-09-030-606-114
; Sequence 114, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:49:45 ; Search time 18.678 Seconds
(without alignments)
97.876 Million cell updates/sec

Title: US-09-780-669-114_COPY_151_169

Perfect score: 106
Sequence: 1 GFTNYTDFSDSPYFKENSA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	106	100.0	241	2 A59262	tetraspan TSPAN-1
2	51	48.1	244	1 I39368	T-cell acute lymph
3	49	46.2	253	2 A59264	tetraspan TSPAN-3
4	46.5	43.9	644	2 E88487	protein Cl3B9.4 [i
5	46	43.4	379	1 RGXLA	GTP-binding regula
6	45	42.5	308	2 AE2960	hypothetical prote
7	45	42.5	319	2 A98323	ABC transporter, p
8	45	42.5	322	2 AB2078	iron(III) dicitrat
9	45	42.5	401	2 H97714	apartate transami
10	45	42.5	431	2 T38260	hypothetical prote
11	45	42.5	648	2 B94139	ABC transporter (p
12	45	42.5	757	2 D95103	x-pro dipeptidyl-p
13	45	42.5	795	2 B97971	x-pro dipeptidyl-p
14	45	42.5	1451	2 I40325	dermonecrotic toxi
15	44.5	42.0	459	2 AD1787	lysine decarboxyla
16	44	41.5	203	2 D84221	hypothetical prote
17	44	41.5	384	2 T44652	UDP-N-acetylglucos
18	44	41.5	1069	2 C95349	Ca2+-transporting
19	44	41.5	1093	2 T08551	Ca2+-transporting
20	43.5	41.0	1941	2 T23979	hypothetical prote
21	43.5	41.0	1943	2 T23986	hypothetical prote
22	43	40.6	98	2 T26932	Ig heavy chain V r
23	43	40.6	238	1 I38016	melanoma-associate
24	43	40.6	245	2 A59258	tetraspan TSPAN-6
25	43	40.6	552	2 T27424	hypothetical prote
26	43	40.6	684	2 T37944	hypothetical prote
27	43	40.6	729	2 F83725	hypothetical prote
28	43	40.6	773	2 A71079	probable transcrip
29	43	40.6	773	2 D75031	hydrogenase expres

30	43	40.6	809	2 S67665	ubiquitin-specific
31	43	40.6	1162	2 T21557	hypothetical prote
32	43	40.6	1599	2 S22737	glucosyltransferas
33	43	40.6	4351	2 T00252	MEGF1 protein - ra
34	42	39.6	59	2 C64024	hypothetical prote
35	42	39.6	243	2 AE1709	FMN-containing NAD
36	42	39.6	245	2 A59260	tetraspan TSPAN-6
37	42	39.6	247	2 T50286	hypothetical prote
38	42	39.6	370	2 F86338	protein F2D10.2 [i
39	42	39.6	402	2 A86194	hypothetical prote
40	42	39.6	458	2 T47389	hypothetical prote
41	42	39.6	567	2 JC4714	alpha-glucosidase
42	42	39.6	644	2 T08340	probable arsenical
43	42	39.6	735	2 AC0858	conserved hypothet
44	41.5	39.2	353	2 AD1384	aldose 1-epimerase
45	41.5	39.2	827	2 S59121	SOX6 protein - mou

ALIGNMENTS

RESULT 1

A59262
tetraspan TSPAN-1 - human
C:Species: Homo sapiens (man)
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59262
R: Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A:Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.
A:Reference number: A59258; MUID:98390278; PMID:9714763
A:Accession: A59262
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-241 <TOD>
A:Cross-references: UNIPROT:O60635; GB:AF054838; NID:G2997740; PIDN:AAC69714.1; PID:G299
C:Genetics:
A:Gene: TSPAN-1
C:Superfamily: CD9 antigen

Query Match 100.0%; Score 106; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. NO. 4.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFSDSPYFKENSA 19
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Db 151 GFTNYTDFSDSPYFKENSA 169

RESULT 2

I39368
T-cell acute lymphoblastic leukemia associated antigen 1 - human
N:Alternate names: cell surface glycoprotein (clone A15); TALLA-1
C:Species: Homo sapiens (man)
C>Date: 23-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 22-Jun-1999
C:Accession: I39368; I54784
R:Emi, N.; Kikaoxi, K.; Seto, M.; Ueda, R.; Saito, H.; Takahashi, T.
Immunogenetics 37, 193-198, 1993
A:Title: Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 superfa
A:Reference number: I39368; MUID:93131291; PMID:8420826
A:Accession: I39368
A:Molecule type: mRNA
A:Residues: 1-244 <RES>
A:Cross-references: GB:D10653; NID:G285900; PIDN:BAA01501.1; PID:G285901
A:Experimental source: immature T cell line HPB-ALL
R:Takagi, S.; Fujikawa, K.; Imai, T.; Fukuhara, N.; Fukudome, K.; Minegishi, M.; Tsuchiy
Int. J. Cancer 61, 706-715, 1995
A:Title: Identification of a highly specific surface marker of T-cell acute lymphoblasti
A:Reference number: I54784; MUID:95286314; PMID:7768645
A:Accession: I54784
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-244 <RE2>

Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological processes
A:Reference number: A75000; MUID:9069613; PMID:9851916
A:Note: See websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/c.elegans/ for more information
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999
A:Accession: E88487
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-644 <STO>
A:Cross-references: UNIPROT:Q09460; GB:chr_III; PIN:AAA62517.1; PID:gc87811; GSPDB:GN000000000
C:Genetics:

A;Gene: malF
A;Map position: linear chromosome
C-Superfamily: inner membrane protein ugpA

C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: H97714
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R: Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A37700; MUID:21442074; PMID:11557893
A:Accession: H97714
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-401 <KUR>
A:Cross-references: UNIPROT:Q92UE7; GB:AE006914; PIDN:AAL02658.1; PID:gl15619162; GSPDB:G
C:Genetics:
C:Superfamily: aspartate transaminase
C:Keywords: aminotransferase

Query Match 42.5%; Score 45; DB 2; Length 401;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKE 16
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Db 60 GFTKYNVEGMPLLKQ 75

RESULT 10
T38260
hypothetical protein SPAC23C4.05c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38260
R:Harris, D.; Squares, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21782
A:Accession: T38260
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-431 <HAR>
A:Cross-references: UNIPROT:O94559; EMBL:Z99753; PIDN:CAB16876.1; GSPDB:GN000066; SPDB:SP
A:Experimental source: strain 972h-; cosmid c23C4
C:Genetics:
A:Gene: SPDB:SPAC23C4.05c
A:Map position: 1
A:Introns: 23/1

Query Match 42.5%; Score 45; DB 2; Length 431;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TNYTDFEDSPYFKE 16
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Db 231 TNYTDFEDSPYFKE 244

RESULT 11
B84139
ABC transporter (permease) BH3914 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: B84139
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira: Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B84139
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-648 <STO>
A:Cross-references: UNIPROT:O9K618; GB:AP001520; GB:BA000004; NID:gl0176401; PIDN:BA8076
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3914

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Best Local Similarity		72.7%;	Pred. No. 44;		
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		:			
Db	332	TDMEDAAYFKE 342			
RESULT 12					
D95103					
X-pro dipeptidyl-peptidase [imported] - Streptococcus pneumoniae (strain TIGR4)					
C:Species: Streptococcus pneumoniae					
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004					
C:Accession: D95103					
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid					
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,					
nson, T.; Hickey, E.K.; Holt, I.E.					
Science 293, 498-506, 2001					
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,					
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.					
A:Reference number: A95000; MUID:21357209; PMID:11463916					
A:Accession: D95103					
A>Status: preliminary					
A:Molecule type: DNA					
A:Residues: 1-757 <KUR>					
A:Cross-references: UNIPROT:Q97RC8; GB:AE005672; PIDN:AAK75021.1; PID:gl14972369; GSPDB:G					
A:Experimental source: strain TIGR4					
C:Gene: SP0894					
C:Superfamily: Lactococcus X-Pro dipeptidyl-peptidase					
Query Match		42.5%;	Score 45;	DB 2;	Length 757;
Best Local Similarity		44.4%;	Pred. No. 53;		
Matches		8;	Conservative	4;	Mismatches 6; Indels 0; Gaps 0;
QY	1	GFTNYTDFEDSPYFKENS 18			
		:			
Db	90	GFSYLVDFEDSDVFRKET 107			
RESULT 13					
B97971					
X-pro dipeptidyl-peptidase (EC 3.4.14.11) [imported] - Streptococcus pneumoniae (strain					
C:Species: Streptococcus pneumoniae					
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004					
C:Accession: B97971					
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; B					
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M					
y, P.; Sun, P.M.; Winkler, M.E.					
J. Bacteriol. 183, 5709-5717, 2001					
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;					
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.					
A:Reference number: A97872; MUID:21423245; PMID:11544234					
A:Accession: B97971					
A>Status: preliminary					
A:Molecule type: DNA					
A:Residues: 1-795 <KUR>					
A:Cross-references: UNIPROT:Q8DQ87; GB:AE007317; PIDN:AAK99598.1; PID:gl15458392; GSPDB:G					
C:Gene: pepXP					
C:Superfamily: Lactococcus X-Pro dipeptidyl-peptidase					
C:Keywords: dipeptidylpeptide hydrolase					
Query Match		42.5%;	Score 45;	DB 2;	Length 795;
Best Local Similarity		44.4%;	Pred. No. 56;		
Matches		8;	Conservative	4;	Mismatches 6; Indels 0; Gaps 0;
QY	1	GFTNYTDFEDSPYFKENS 18			
		:			
Db	128	GFSYLVDFEDSDVFRKET 145			

Query Match		42.5%;	Score 45;	DB 2;	Length 1451;
Best Local Similarity		57.1%;	Pred. No. 1.1e+02;		
Matches		8;	Conservative	2;	Mismatches 4; Indels 0; Gaps 0;
QY	1	GFTNYTDFEDSPYF 14			
		:			
Db	427	GFISFTDFRSDAF 440			
RESULT 15					
AD1787					
lysine decarboxylase homolog lin2842 [imported] - Listeria innocua (strain Clip1					
C:Species: Listeria innocua					
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 28-Jul-2003					
C:Accession: AD1787					
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; B					
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F					
D.; Jones, L.M.; Karst, U.					
Science 294, 849-852, 2001					
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournan					
ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.;					
A:Title: Comparative genomics of Listeria species.					
A:Reference number: AB1077; MUID:21537279; PMID:11679669					
A:Accession: AD1787					
A>Status: preliminary					
A:Molecule type: DNA					
A:Residues: 1-459 <GLA>					
A:Cross-references: GB:AL592022; PIDN:CAC98068.1; PID:gl16415377; GSPDB:GN00178					
A:Experimental source: strain Clip11262					
C:Genetics:					
A:Gene: lin2842					
C:Superfamily: lysine decarboxylase					
Query Match		42.0%;	Score 44.5;	DB 2;	Length 459;
Best Local Similarity		52.6%;	Pred. No. 36;		
Matches		10;	Conservative	2;	Mismatches 4; Indels 3; Gaps 1;
QY	1	GFTNY---TDFEDSPYFKE 16			
		:			
Db	316	GYTGVELQTFIESSYPPE 334			
Search completed: February 5, 2005, 20:05:44					
Job time : 20.678 secs					

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:36:20 ; Search time 90.1695 Seconds
(without alignments)
107.902 Million cell updates/sec

Title: US-09-780-669-114_COPY_151_169
Perfect score: 106
Sequence: 1 GFTNYTDFSDSPYFKENSA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	241	1	TSN1_HUMAN
2	62	58.5	241	2	O6AYR9 rattus norv
3	60	56.6	240	2	O99J59 mus musculu
4	56	52.8	248	2	O810P9 mus musculu
5	52	49.1	96	2	Q7VAG9 Qvrag9 prochloroco
6	51	48.1	52	2	Q7Z215 homo sapien
7	51	48.1	52	2	Q7YQH1 pan troglod
8	51	48.1	52	2	Q7YQH2 pan troglod
9	51	48.1	240	2	O6GP11 xenopus lae
10	51	48.1	244	1	T4S2_PANTR
11	51	48.1	244	1	T4S2_PONPY
12	51	48.1	244	2	Q7Z326
13	51	48.1	249	1	T4S2_HUMAN
14	50	47.2	433	2	O89XR2 Q89xr2 bradyrhizob
15	50	47.2	434	2	O6N118 rhodopsendo
16	50	47.2	728	2	Q9UWN8 sulfolobu
17	49	46.2	157	2	Q8R0G6 mus musculu
18	49	46.2	235	2	Q7RD42
19	49	46.2	240	2	Q6P420 xenopus lae
20	49	46.2	244	2	O6PDN6 mus musculu
21	49	46.2	244	2	O6DDV1 xenopus lae
22	49	46.2	245	2	Q8BPV2 mus musculu
23	49	46.2	249	1	T4S2_MOUSE
24	49	46.2	253	1	T4S2_HUMAN
25	49	46.2	253	1	T4S8_MOUSE
26	49	46.2	253	2	O66H06 rattus norv
27	49	46.2	254	2	O8ILA9 plasmodium
28	49	46.2	254	2	Q89GR4 bradyrhizob
29	48.5	45.8	234	2	Q7T2B8 brachydanio
30	48	45.3	157	2	Q9GMU7 macaca fasc
31	48	45.3	506	2	Q8S2J1 oryza sativ

32	48	45.3	790	2	Q6FR86
33	47	44.3	186	2	Q8R8J0
34	47	44.3	194	2	Q67QV1
35	47	44.3	328	2	Q976G5
36	47	44.3	340	2	Q95XX8
37	46.5	43.9	495	2	Q8PSR6
38	46	43.4	109	2	Q9L7X0
39	46	43.4	258	2	Q94F78
40	46	43.4	271	2	Q89PE4
41	46	43.4	299	2	Q88TV7
42	46	43.4	323	2	Q7Q3Z8
43	46	43.4	379	1	GBAS_XENLA
44	46	43.4	384	2	Q7MZG8
45	46	43.4	412	2	Q8XJJ0

ALIGNMENTS

RESULT 1
TSN1_HUMAN
ID TSN1_HUMAN STANDARD; PRT; 241 AA.
AC O60635; O60745;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Tetraspanin 1 (Tspan-1) (Tetraspanin NET-1) (Tetraspanin TM4-C).
GN Name=TSPAN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98390278; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6;
RA Todd S.C., Doctor V.S., Levy S.;
RT "Sequences and expression of six new members of the tetraspanin/TW4SF family.";
RL Biochim. Biophys. Acta 1399:101-104(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Rubinstein E., Serru V., Boucheix C.;
RT "New tetraspans identified in the EST database.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Puls K.L., Ni J., Liu D., Morahan G., Wright M.D.;
RT "The molecular characterization of four tetraspans.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=42388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Fahney J., Helton E., Kettelman M., Madao A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Gough J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Abramson R.D., Mullaly S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Grouse L.H., Derge J.G.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RL SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RC Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC078938; AAH78938.1; -
 DR GO: GO:0015021; C:integral to membrane; IEA.
 DR InterPro: IPR002229; RhesusRHD
 DR InterPro: IPR008952; Tetraspanin.
 DR InterPro: IPR000301; Transmem 4.
 DR Pfam: PF00335; Tetraspanin; 1.
 DR PRINTS: PR00342; RHESUSRHD.
 DR PRINTS: PR00259; TMFOUR.
 DR PROSITE: PS00421; TM4_1; 1.
 DR SQ SEQUENCE 241 AA; 26453 MW; 9118B865464D1A70 CRC64;

 Query Match 58.5%; Score 62; DB 2; Length 241;
 Best Local Similarity 64.7%; Pred. No. 0.15;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps

 Qy 1 GFTNYTDFSDSPYFKEN 17
 || ||||| : |||
 Db 151 GFNNYTFDNSRFVKEN 167

 RESULT 3
 Q99J59 PRELIMINARY; PRT; 240 AA.
 ID Q99J59
 AC Q99J59;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE RIKEN cDNA 9030418M05 (Mus musculus adult male colon cDNA, RIKEN full-
 DE length enriched library, clone:9030418M05 product:similar to tetraspan-
 DE TSPAN-1).
 DE Name=9030418M05Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinus K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RL SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RC Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC078938; AAH78938.1; -
 DR GO: GO:0015021; C:integral to membrane; IEA.
 DR InterPro: IPR002229; RhesusRHD
 DR InterPro: IPR008952; Tetraspanin.
 DR InterPro: IPR000301; Transmem 4.
 DR Pfam: PF00335; Tetraspanin; 1.
 DR PRINTS: PR00342; RHESUSRHD.
 DR PRINTS: PR00259; TMFOUR.
 DR PROSITE: PS00421; TM4_1; 1.
 DR SQ SEQUENCE 241 AA; 26453 MW; 9118B865464D1A70 CRC64;

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami T., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN EMBL; BC003448; AA003448.1; -;
DR EMBL; AK078869; BAC37431.1; -;
DR MGD; MGI:1914055; 9030418M05R1K.

DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00342; RHESUSRHD.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
SQ SEQUENCE 240 AA; 26356 MW; AD4C448A32BC2999 CRC64;

Query Match 56.6%; Score 60; DB 2; Length 240;
Best Local Similarity 64.7%; Pred. No. 0.32;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKEN 17
||| ||||| : |||
Db 151 GFNNYTDNFASRFVKEN 167

RESULT 4
Q810P9 PRELIMINARY; PRT; 248 AA.
AC Q810P9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049650; AA049650.1; -;
GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00259; TMFOUR.
KW Hypothetical protein.
SQ SEQUENCE 248 AA; 27877 MW; F89C7B36382E2C5B CRC64;

Query Match 52.8%; Score 56; DB 2; Length 248;
Best Local Similarity 64.3%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GFTNYTDFEDSPYF 14
DB 144 GVKNYTDWNDNPFYF 157

RESULT 5
Q7VAG9 PRELIMINARY; PRT; 96 AA.
AC Q7VAG9; 2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Homolog of PabF protein.
GN OrderedLocusNames=Pro1494;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
SEQUENCE FROM N.A.
STEAIN=SARG / COMP 1375 / SS120;
MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufrene A., Salanoubat M., Fartensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal oxyphototrophic genome."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).
DR EMBL; AE017165; AAQ00538.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009539; C:photosystem II reaction center; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006216; CYC_B559.
DR InterPro; IPR006241; CYC_B559_beta.
DR Pfam; PF00283; Cytochrom B559; 1.
DR ProDom; PD004747; CYC_b559_beta; 1.
DR Complete proteome.
KW SEQUENCE 96 AA; 10905 MW; B07816D33A1161AA CRC64;

Query Match 49.1%; Score 52; DB 2; Length 96;
Best Local Similarity 58.8%; Pred. No. 2;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKN 17
DB 37 GFENYQDWEDSGVTPEN 53

RESULT 6
Q7Z215 PRELIMINARY; PRT; 52 AA.
AC Q7Z215; 2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transmembrane 4 superfamily member 2 (Fragment).
GN Name=TM4SF2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
RT chimpanzees."
RL Mol. Biol. Evol. 20:1281-1289 (2003).
DR EMBL; AB102461; BAC80930.1; -

QY 1 GFTNYTDFEDSPYFKN 17
DB 5 GVNQYTNWSTSPYFLEH 21

RESULT 7
Q7YQH1 PRELIMINARY; PRT; 52 AA.
AC Q7YQH1; 2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transmembrane 4 superfamily member 2 (Fragment).
GN Name=TM4SF2;
OS Pan troglodytes verus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=37012;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
RT chimpanzees."
RL Mol. Biol. Evol. 20:1281-1289 (2003).
DR EMBL; AB102481; BAC80950.1; -
DR EMBL; AB102482; BAC80951.1; -
DR EMBL; AB102483; BAC80952.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem_4.
DR Transmembrane.
FT NON_TER 1 1
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5774 MW; 420AB346A5074DC8 CRC64;

Query Match 48.1%; Score 51; DB 2; Length 52;
Best Local Similarity 52.9%; Pred. No. 1.4;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKN 17
DB 5 GVNQYTNWSTSPYFLEH 21

RESULT 7
Q7YQH1 PRELIMINARY; PRT; 52 AA.
AC Q7YQH1; 2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transmembrane 4 superfamily member 2 (Fragment).
GN Name=TM4SF2;
OS Pan troglodytes verus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=37012;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
RT chimpanzees."
RL Mol. Biol. Evol. 20:1281-1289 (2003).
DR EMBL; AB102462; BAC80931.1; -
DR EMBL; AB102463; BAC80932.1; -
DR EMBL; AB102464; BAC80933.1; -
DR EMBL; AB102465; BAC80934.1; -
DR EMBL; AB102466; BAC80935.1; -
DR EMBL; AB102467; BAC80936.1; -
DR EMBL; AB102468; BAC80937.1; -
DR EMBL; AB102469; BAC80938.1; -
DR EMBL; AB102470; BAC80939.1; -
DR EMBL; AB102471; BAC80940.1; -
DR EMBL; AB102472; BAC80941.1; -
DR EMBL; AB102473; BAC80942.1; -
DR EMBL; AB102474; BAC80943.1; -
DR EMBL; AB102475; BAC80944.1; -
DR EMBL; AB102476; BAC80945.1; -
DR EMBL; AB102477; BAC80946.1; -
DR EMBL; AB102478; BAC80947.1; -
DR EMBL; AB102479; BAC80948.1; -
DR EMBL; AB102480; BAC80949.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem_4.
DR Transmembrane.
FT NON_TER 1 1
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5774 MW; 420AB346A5074DC8 CRC64;

Query Match 48.1%; Score 51; DB 2; Length 52;
Best Local Similarity 52.9%; Pred. No. 1.4;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKN 17
DB 5 GVNQYTNWSTSPYFLEH 21

RESULT 7
Q7YQH1 PRELIMINARY; PRT; 52 AA.
AC Q7YQH1; 2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transmembrane 4 superfamily member 2 (Fragment).
GN Name=TM4SF2;
OS Pan troglodytes verus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=37012;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
RT chimpanzees."
RL Mol. Biol. Evol. 20:1281-1289 (2003).
DR EMBL; AB102461; BAC80930.1; -

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Db 5 GVQNTNWTSTSPYFLEH 21

RESULT 8

Q7YQH2 PRELIMINARY; PRT; 52 AA.

AC Q7YQH2

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Transmembrane 4 superfamily member 2 (Fragment).

GN Name=TW4SP2;

OS Pan troglodytes troglodytes.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

OX NCBI_TaxID=37011;

RN [1]

RP SEQUENCE FROM N.A.

EX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;

RA Kitano T., Schwarz C., Nickel B., Paabo S.;

RT "Gene diversity patterns at 10 X-chromosomal loci in humans and chimpanzees.";

RL Mol. Biol. Evol. 20:1281-1289(2003).

DR EMBL; AB102484; BAC80953.1; -

DR EMBL; AB102485; BAC80954.1; -

DR EMBL; AB102486; BAC80955.1; -

DR EMBL; AB102487; BAC80956.1; -

DR EMBL; AB102488; BAC80957.1; -

DR EMBL; AB102489; BAC80958.1; -

DR EMBL; AB102490; BAC80959.1; -

DR GO; GO:0016021; C: integral to membrane; IEA.

DR InterPro; IPR008952; Tetraspanin.

DR InterPro; IPR00301; Transmem. 4.

KW Transmembrane.

FT NON_TER 1 1

FT NON_TER 52 52

SQ SEQUENCE 52 AA; 5774 MW; 420AB346A5074DC8 CRC64;

Query Match 48.1%; Score 51; DB 2; Length 52;

Best Local Similarity 52.9%; Pred. No. 1.4;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GFTNYTDFSPYFLEN 17

Db 5 GVQNTNWTSTSPYFLEH 21

RESULT 9

Q6GP11 PRELIMINARY; PRT; 240 AA.

AC Q6GP11

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE MGC80751 protein.

GN Name=MGC80751;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Splicein;

EX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Splicein;

EX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus RT initiative.";

RL Dev. Dyn. 225:384-391(2002).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Splicein;

RA Klein S., Gerhard D.S.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.

DR EMBL; BC073338; AAH73338.1; -

DR GO; GO:0016021; C: integral to membrane; IEA.

DR InterPro; IPR008952; Tetraspanin.

DR InterPro; IPR00301; Transmem. 4.

DR Pfam; PF00335; Tetraspanin; 1.

DR PRINTS; PR00259; TMFOUR.

SQ SEQUENCE 240 AA; 26875 MW; 96475F0A8F920998 CRC64;

Query Match 48.1%; Score 51; DB 2; Length 240;

Best Local Similarity 42.1%; Pred. No. 8.4;

Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GFTNYTDFSPYFENKSA 19

Db 146 GRKNTDWEETDWTNNKS 164

RESULT 10

T4S2 PANTR

ID T4S2 PANTR STANDARD; PRT; 244 AA.

AC Q7YQL0;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Transmembrane 4 superfamily member 2.

GN Name=TW4SP2;

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

OX NCBI_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

EX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;

RA Kitano T., Schwarz C., Nickel B., Paabo S.;

RT "Gene diversity patterns at 10 X-chromosomal loci in humans and chimpanzees.";

RL Mol. Biol. Evol. 20:1281-1289(2003).

CC -!- FUNCTION: May be involved in cell proliferation and cell motility.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to the tetraspanin (TW4SP) family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC -----
DR EMBL; AB102666; BAC81135.1; -.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Transmembrane.
FT DOMAIN 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 35 Potential.
FT DOMAIN 36 51 Extracellular (Potential).
FT TRANSMEM 52 70 Potential.
FT DOMAIN 71 81 Cytoplasmic (Potential).
FT TRANSMEM 82 107 Extracellular (Potential).
FT DOMAIN 108 209 Potential.
FT TRANSMEM 209 229 Potential.
FT DOMAIN 230 244 Cytoplasmic (Potential).
FT CARBOHYD 49 49 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 150 150 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 153 153 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 183 183 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 244 AA; 26972 MW; 53B003EB5A8A202C CRC64;

Query Match 48.1%; Score 51; DB 1; Length 244;
Best Local Similarity 52.9%; Pred. No. 8.5;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKEN 17
DB 147 GVQNYTNWSTSPYFLEH 163

RESULT 11
T4S2_PONPY STANDARD; PRT; 244 AA.
AC Q7YOK9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transmembrane 4 superfamily member 2.
GN Name=TW4SF2;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and chimpanzees.";
RL Mol. Biol. Evol. 20:1281-1289(2003).
DR EMBL; AB102667; BAC81136.1; -.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Transmembrane.
FT DOMAIN 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 35 Potential.
FT DOMAIN 36 51 Extracellular (Potential).
FT TRANSMEM 52 70 Potential.

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-----
EMBL; AB102667; BAC81136.1; -.
InterPro; IPR000301; Transmem 4.
Pfam; PF00335; Tetraspannin; 1.
PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Transmembrane.
FT DOMAIN 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 35 Potential.
FT DOMAIN 36 51 Extracellular (Potential).
FT TRANSMEM 52 70 Potential.
```

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FT DOMAIN 71 81 Cytoplasmic (Potential).
FT TRANSMEM 82 107 Potential.
FT DOMAIN 108 209 Extracellular (Potential).
FT TRANSMEM 209 229 Potential.
FT DOMAIN 230 244 Cytoplasmic (Potential).
FT CARBOHYD 49 49 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 150 150 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 153 153 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 183 183 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 244 AA; 26945 MW; 656EA949EE190508 CRC64;

Query Match 48.1%; Score 51; DB 1; Length 244;
Best Local Similarity 52.9%; Pred. No. 8.5;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKEN 17
DB 147 GVQNYTNWSTSPYFLEH 163

RESULT 12
Q7Z3Z6 PRELIMINARY; PRT; 244 AA.
AC Q7Z3Z6;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Transmembrane 4 superfamily member 2.
GN Name=TM4SF2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and chimpanzees.";
RL Mol. Biol. Evol. 20:1281-1289(2003).
DR EMBL; AB102665; BAC81134.1; -.
DR InterPro; IPR008952; Tetraspannin.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; 1.
DR PROSITE; PS00421; TM4_1; UNKNOWN_1.
KW Transmembrane.
SQ SEQUENCE 244 AA; 26972 MW; 53B003EB5A8A202C CRC64;

Query Match 48.1%; Score 51; DB 2; Length 244;
Best Local Similarity 52.9%; Pred. No. 8.5;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKEN 17
DB 147 GVQNYTNWSTSPYFLEH 163

RESULT 13
T4S2_HUMAN STANDARD; PRT; 249 AA.
AC P41732; Q8WVG5; Q9UEY9;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transmembrane 4 superfamily member 2 (Cell surface glycoprotein A15)
DE (T-cell acute lymphoblastic leukemia associated antigen 1) (TALLA-1)
DE (Membrane component, X chromosome, surface marker 1) (CD231 antigen).
GN Name=TM4SF2; Synonyms=A15, MXS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```


RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Matanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohata M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AF005935; BAC45510.1; -.
DR HSSP; P13254; 1GCO.
DR GO; GO:0016829; F-lyase activity; IEA.
DR GO; GO:0016765; F:transferase activity, transferring alkyl or. . .; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR000277; Cys Met Meta PP.
DR InterPro; IPR006235; OAH_OAS_sulphy.
DR Pfam; PF01053; Cys Met Meta PP; 1.
DR TIGRFAMs; TIGR01326; OAH_OAS_sulphy; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 433 AA; 46823 MW; 5A4110C4615F70B5 CRC64;

Query Match 47.2%; Score 50; DB 2; Length 433;
Best Local Similarity 61.5%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 FTNYTDFEDSPYF 14
Db : ||| | ||| :
313 WNYTGFDPSPY 325

RESULT 15
Q6N118
ID Q6N118 PRELIMINARY; PRT; 434 AA.
AC Q6N118;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Homocysteine synthase (EC 2.5.1.49).
GN Names: metY; Ordered Locus Names: RPA4591;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres Y. Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572607; CAE30031.1; -.
DR GO; GO:0003981; P:O-acetylhomoserine aminocarboxypropyltransf. . .; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR000277; Cys Met Meta PP.
DR InterPro; IPR006235; OAH_OAS_sulphy.
DR Pfam; PF01053; Cys Met Meta PP; 1.
DR TIGRFAMs; TIGR01326; OAH_OAS_sulphy; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 434 AA; 46947 MW; B7846EA96BA911FC CRC64;

Query Match 47.2%; Score 50; DB 2; Length 434;
Best Local Similarity 61.5%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 FTNYTDFEDSPYF 14
Db : ||| | ||| :
313 WNYTGFDPSPY 325

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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:34:18 ; Search time 104.746 Seconds
(without alignments)
73.847 Million cell updates/sec

Title: US-09-780-669-114_COPY_165_184
Perfect score: 116
Sequence: 1 KENSAFPFCCNDNVNTAN 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	20	4	AAM01158 Human pro
2	116	100.0	20	4	AAU69803 Human pro
3	116	100.0	20	4	AAG99043 Human pro
4	116	100.0	20	4	ABU71694 Prostate
5	116	100.0	20	5	ABB95263 Epitope m
6	116	100.0	20	6	ABR54375 Prostate
7	116	100.0	20	7	ADBI3955 Human pro
8	116	100.0	20	7	ADG26371 Human pro
9	116	100.0	172	7	ADG69590 Human REM
10	116	100.0	174	8	ADP81123 Protein o
11	116	100.0	214	8	ADR65994 Human pro
12	116	100.0	214	8	ADR68892 Human pro
13	116	100.0	233	6	AAW75060 Human sec
14	116	100.0	233	6	ABO01936 Novel hum
15	116	100.0	240	4	AAAG62153 Human pol
16	116	100.0	240	5	ABB89113 Human pol
17	116	100.0	241	2	AAW63386 Prostate
18	116	100.0	241	2	AAW59954 Amino aci
19	116	100.0	241	2	AAW71870 Amino aci
20	116	100.0	241	2	AAW58380 Human sec
21	116	100.0	241	3	AAW82003 Human imm
22	116	100.0	241	3	ABG94412 Human pro
23	116	100.0	241	4	AAW01118 Human pro
24	116	100.0	241	4	AAU69764 Human pro
25	116	100.0	241	4	AAW74801 Prostate

26	116	100.0	241	4	AAG99003 Human pro
27	116	100.0	241	4	ABU71654 Prostate
28	116	100.0	241	4	AAU04962 Human pro
29	116	100.0	241	4	AAU04962 Human pro
30	116	100.0	241	5	ABG96434 Human ova
31	116	100.0	241	5	ABB95223 Human NI-
32	116	100.0	241	5	ABG76666 Prostate
33	116	100.0	241	6	ABR54335 Prostate
34	116	100.0	241	7	ADBI3564 Human pro
35	116	100.0	241	7	ADG25980 Human pro
36	116	100.0	241	7	ADG25980 Human pro
37	116	100.0	241	7	ADN33286 Cancer/fan
38	116	100.0	258	5	ABG96433 Human ova
39	116	100.0	258	7	ADBI3564 Human ova
40	116	100.0	273	2	AAW61618 Clone HPW
41	116	100.0	273	7	ABW01500 Human rec
42	50	43.1	241	5	ABB09512 Human TSP
43	50	43.1	241	8	ADO10063 Novel hum
44	50	43.1	301	7	ADG44848 S. solfat
45	50	43.1	301	7	ADG42862 S. solfat

ALIGNMENTS

RESULT 1
AAM01158
ID AAM01158 standard; peptide; 20 AA.
XX
AC AAM01158;
XX
DT 04-OCT-2001 (first entry)
XX
DS Human prostate-specific peptide used in epitope mapping studies #15.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX
KW cytosolic; gene therapy; metastasis.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001574.
XX
PR 14-JAN-2000; 2000US-00483672.
XX
(CORI-) CORIXA CORP.
XX
XU J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XU Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
XU Wang A, Meagher MJ;
XU WPI; 2001-425873/45.
XX
DR New polynucleotide encoding a prostate-specific protein, for diagnosing,
XX
PT monitoring and treating prostate cancer in a patient and for use in
XX
PT vaccines.
XX
FS Claim 2; Page 399; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
XX
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX
CC and can be used in vaccine production and gene therapy. (I), (II),
XX
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
XX
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
XX
CC the antibodies are also used in the detection of cancer in a patient. The
XX
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
XX
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
XX
CC monitoring the progression of cancer in a patient. (I) and (II) can also
XX
CC be used to improve diagnostic and therapeutic methods for prostate
XX
CC cancer. They can indicate the level of metastasis as well as the prostate

CC	antigenic epitopes or domains of prostate specific proteins					
XX						
SX	Sequence 20 AA;					
	Query Match	100.0%;	Score 116;	DB 4;	Length 20;	
	Best Local Similarity	100.0%;	Pred. No. 3.9e-10;	Mismatches	0;	Gaps 0;
	Matches	20;	Conservative	0;	Indels	0;
QY	1 KENSAPPPFCNDNVNTNAN 20 					
Db	1 KENSAPPPFCNDNVNTNAN 20 					
RESULT 3						
AAG99043	AAG99043 standard; peptide; 20 AA.					
ID	AAG99043					
XX	AC AC					
XX	AAG99043;					
XX	XX XX					
DT	25-SEP-2001 (first entry)					
XX	Human prostate-specific epitope mapping peptide #15.					
DE	XX XX					
XX	Human; prostate cancer; therapy; diagnosis; cat eye syndrome;					
XX	chromosome 22q11.2; prostate-specific protein; chromosome 1;					
KW	prostate specific antigen; PSA.					
KW	KW KW					
XX	XX XX					
OS	Homo sapiens.					
XX	WO200134802-A2.					
PN	17-MAY-2001.					
PD	XX XX					
XX	O9-NOV-2000; 2000WO-US030904.					
PF	XX XX					
PR	12-NOV-1999; 99US-00439313.					
PR	18-NOV-1999; 99US-00443686.					
XX	XX XX					
PA	(CORI-) CORIXA CORP.					
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;					
PI	Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;					
XX	WPI; 2001-308785/32.					
DR	Isolated polypeptide comprising at least an immunogenic portion of a					
PT	prostate-specific protein, useful in the diagnosis and therapy of					
PT	prostate cancer.					
XX	Claim 3; Page 299; 325pp; English.					
PS	XX XX					
XX	The present invention describes an isolated polypeptide (Pl) comprising					
CC	at least an immunogenic portion of a prostate-specific protein, or its					
CC	variant. Also described are polynucleotides (N1) encoding (Pl). (Pl) and					
CC	(N1) have cytostatic activity and can be used in vaccine production. The					
CC	polypeptides, nucleic acids and antibodies from the present invention are					
CC	useful in the diagnosis and therapy of prostate cancer. Prostate specific					
CC	genes P704P, P712P, P774P, P775P and B305D are located in a genomic					
CC	region on chromosome 22q11.2 known as the Cat Eye Syndrome region.					
CC	Prostate specific antigen (PSA) P501S was located on chromosome 1.					
CC	AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide.					
CC	and polypeptide sequences used in the exemplification of the present					
CC	invention					
XX	XX XX					
SQ	Sequence 20 AA;					
	Query Match	100.0%;	Score 116;	DB 4;	Length 20;	
	Best Local Similarity	100.0%;	Pred. No. 3.9e-10;	Mismatches	0;	Gaps 0;
	Matches	20;	Conservative	0;	Indels	0;
Qy	1 KENSAPPPFCNDNVNTNAN 20 					
Db	1 KENSAPPPFCNDNVNTNAN 20 					

RESULT 4

ABU71694
ID ABU71694 standard; peptide; 20 AA.

XX AC ABU71694;

XX DT 10-JUN-2003 (first entry)

XX DE Prostate cancer therapy associated peptide #16.

XX KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA.

XX OS Homo sapiens.

XX PN US2002192763-A1.

XX PD 19-DEC-2002.

XX PF 29-JUN-2001; 2001US-00895793.

XX PR 04-OCT-1999; 99US-0157455P.

XX PR 04-OCT-2000; 2000US-00679272.

XX PR 28-MAR-2001; 2001US-00822827.

XX PA (XUJJ/) XU J.

XX PA (DILL/) DILLON D C.

XX PA (MITC/) MITCHAM J L.

XX PA (HARL/) HARLOCKER S L.

XX PA (JIAN/) JIANG Y.

XX PA (KALO/) KALOS M D.

XX PA (FANG/) FANGER G R.

XX PA (RETT/) RETTER M W.

XX PA (STOL/) STOLK J A.

XX PA (DAYC/) DAY C H.

XX PA (VEDV/) VEDVICK T S.

XX PA (CART/) CARTER D.

XX PA (LISX/) LI S X.

XX PA (WANG/) WANG A.

XX PA (SKEI/) SKEIKY Y A W.

XX PA (HEPL/) HEPLER W T.

XX PA (HEND/) HENDERSON R A.

XX PA (HURA/) HURAL J.

XX PA (MCNE/) MCNEILL P D.

XX PA (HOUG/) HOUGHTON R L.

XX PA (DBAS/) Y DE BASSOLS C V.

XX PA (FOYT/) FOY T M.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;

PI McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;

XX WPI; 2001-245062/25.

XX PT Prostate specific protein and its encoding polynucleotide, useful for the

PT treatment and diagnosis of prostate cancer.

XX PS Example 18; SEQ ID NO 505; 85pp; English.

XX CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This is the amino acid sequence of a

CC prostate cancer therapy associated peptide. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?docID=US20020192763

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 116; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPFCNDNVNTAN 20

Db 1 KENSAPPPFCNDNVNTAN 20

RESULT 5

ABB95263

ID ABB95263 standard; peptide; 20 AA.

XX AC ABB95263;

XX DT 19-JUL-2002 (first entry)

XX DE Epitope mapping study peptide SEQ ID NO 505.

XX KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX KW gene therapy.

XX OS Unidentified.

XX PN US2002022248-A1.

XX PD 21-FEB-2002.

XX PF 12-JAN-2001; 2001US-00759143.

XX PR 25-FEB-1997; 97US-00806099.

XX PR 01-AUG-1997; 97US-00904804.

XX PR 10-FEB-1998; 98US-00020956.

XX PR 25-FEB-1998; 98US-00030607.

XX PR 14-JUL-1998; 98US-00115453.

XX PR 23-SEP-1998; 98US-00159812.

XX PR 15-JAN-1999; 99US-00232149.

XX PR 09-APR-1999; 99US-00288946.

XX PR 13-JUL-1999; 99US-00352616.

XX PR 12-NOV-1999; 99US-00439313.

XX PR 18-NOV-1999; 99US-00443686.

XX PR 14-JAN-2000; 2000US-00483672.

XX PR 27-MAR-2000; 2000US-00536857.

XX PR 09-MAY-2000; 2000US-00568100.

XX PR 12-MAY-2000; 2000US-00570737.

XX PR 13-JUN-2000; 2000US-00593793.

XX PR 27-JUN-2000; 2000US-00605783.

XX PR 10-AUG-2000; 2000US-00636215.

XX PR 29-AUG-2000; 2000US-00651236.

XX PR 06-SEP-2000; 2000US-00657279.

XX PR 02-OCT-2000; 2000US-00679426.

XX PR 10-OCT-2000; 2000US-00685166.

XX PA (XUJJ/) XU J.

XX PA (DILL/) DILLON D C.

XX PA (MITC/) MITCHAM J L.

XX PA (HARL/) HARLOCKER S L.

XX PA (JIAN/) JIANG Y.

XX PA (KALO/) KALOS M D.

XX PA (FANG/) FANGER G R.

XX PA (RETT/) RETTER M W.

XX PA (STOL/) STOLK J A.

XX PA (DAYC/) DAY C H.

XX PA (VEDV/) VEDVICK T S.

XX PA (CART/) CARTER D.

XX PA (LISX/) LI S X.

PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
XX Claim 2; SEQ ID NO 505; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a
CC peptide described in the invention
XX
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 116; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-10; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 1 KENSAPPPFCNDNVNTAN 20
Db 1 KENSAPPPFCNDNVNTAN 20
RESULT 6
ABR54375
ID ABR54375 standard; protein; 20 AA.
AC ABR54375;
XX
XX 28-AUG-2003 (first entry)
DT
XX
XX Prostate tumour specific related peptide for epitope mapping SEQ ID 505.
DE
XX
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
XX immune response; prostate cancer.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200289747-A2.
FN
XX
XX 14-NOV-2002.
PD
XX
XX 09-MAY-2002; 2002WO-US014753.
PF
XX
XX 09-MAY-2001; 2001US-00852911.
PR
XX 29-JUN-2001; 2001US-00895814.
PR
XX 10-DEC-2001; 2001US-00012896.
PR
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Deng T;
XX
XX WPI; 2003-167130/16.
DR
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
XX particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
PT
XX
XX

PS Example 18; Page 466; 691pp; English.
XX
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 116; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-10; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 1 KENSAPPPFCNDNVNTAN 20
Db 1 KENSAPPPFCNDNVNTAN 20
RESULT 7
ABR13955
ID ABR13955 standard; peptide; 20 AA.
XX
XX ABR13955;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Human prostate protein P503S epitope mapping peptide #2102.
DE
XX
XX Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
KW cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell; epitope.
XX
XX
XX Homo sapiens.
OS
XX
XX US2003185830-A1.
PN
XX
XX 02-OCT-2003.
PD
XX
XX 12-NOV-2002; 2002US-00294025.
PF
XX
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX

PA (CORI-) CORIXA CORP.
XX Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
XX
PT New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
PS Example 18; Page; 101pp; English.
XX
CC The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
CC peptides comprise a fragment ADBI3563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADBI3563, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is an epitope or
CC peptide derived from one of the prostate specific proteins of the
CC invention. Note: Except where otherwise indicated, the sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030185630.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 116; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-10; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KENSAPPPFCNDNVNTAN 20
Db 1 KENSAPPPFCNDNVNTAN 20
RESULT 8
ADG26371
XX ADG26371 standard; peptide; 20 AA.
XX AC ADG26371;
XX DT 26-FEB-2004 (first entry)
XX DE Human prostate-specific polypeptide #44.
XX KW Human; prostate-specific polypeptide; prostate cancer; cytostatic.
XX OS Homo sapiens.

XX US2003157089-A1.
XX 21-AUG-2003.
XX
XX 09-MAY-2002; 2002US-00144678.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.
XX 09-FEB-2001; 2001US-00780669.
XX 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-008595814.
XX 10-DEC-2001; 2001US-00012896.
XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
XX Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
XX Carter D, Li SX, Wang A, Skelky YAM, Hepler WT, Hural J;
XX McNeill PD, Houghton RL, Vinals Y De Bassolec, Foy TM, Watanabe Y;
XX Mesgher MJ, Deng T;
XX WPI; 2003-777973/73.

XX New polynucleotides encoding prostate specific polypeptides isolated from
XX a human prostate tumor cDNA library are useful to diagnose and treat
XX cancer particularly prostate cancer.

XX Example 18; SEQ ID NO 505; 99pp; English.

XX The invention relates to human prostate-specific polypeptides and the
XX polynucleotides encoding them. The invention also relates to an isolated
XX antibody or its antigen-binding fragment that specifically binds a
XX polypeptide of the invention, a method of detecting cancer in a patient
XX comprising contacting a biological sample of the patient with an agent
XX that binds a prostate-specific polypeptide and comparing the amount of
XX bound polypeptide compared to a predetermined cut-off value and a fusion
XX protein comprising a prostate-specific polypeptide. The sequences of the
XX invention are used to diagnose and treat cancer, particularly prostate
XX cancer. This sequence represents a human prostate-specific polypeptide of
XX the invention. Note: The sequence data for this patent did not form part
XX of the printed specification but was obtained in electronic format
XX directly from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 20 AA;

XX Query Match 100.0%; Score 116; DB 7; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPFCNDNVNTAN 20

Db 1 KENSAPFPCCNDNVNTAN 20
|||||

RESULT 9
ADD69590
ID ADD69590 standard; protein; 172 AA.

XX AC ADD69590;

XX DT 15-JAN-2004 (first entry)

XX DE Human REMAP protein - SEQ ID 19.

XX DE human; receptor and membrane-associated protein; REMAP; cytostatic;
KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
KW thromimetic; cell proliferative; cancer; atherosclerosis; neurological;
KW epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS;
KW allergy; developmental; hypothyroidism; Cushing's syndrome; infection.

XX OS Homo sapiens.

XX PN W02003048305-A2.

XX PD 12-JUN-2003.

XX PF 13-NOV-2002; 2002WO-US036759.

XX PR 13-NOV-2001; 2001US-0333097P.

XX PR 15-NOV-2001; 2001US-0335274P.

XX PR 14-DEC-2001; 2001US-0340542P.

XX PR 18-DEC-2001; 2001US-0342166P.

XX PR 11-JAN-2002; 2002US-0347580P.

XX PR 14-JAN-2002; 2002US-0348687P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Duggan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y,
PI Chawla NK, Warren BA, Barroso I, Becha SD, Yue H, Lehr-Mason PM;
PI Thangavelu K, Lee S, Emerling BM, Kable AE, Khare R, Baughn MR;
PI Gandhi AR, Tran UK, Richardson TW, Marquis JP, Lal PG, Forsythe IJ;
PI Lee EA, Swarnakar A, Kallick DA, Griffin JA, Elliott VS, Gorvad AE;
PI Hatalla AA, Ison CH, Jin P, Jiang X, Jackson AA, Bhatia U;
PI Burrill JD, Blake JJ, Ho A, Zheng W, Gao J;

XX WPI; 2003-513744/48.

XX DR N-PSDB; ADD69637.

XX PT New human receptors and membrane-associated proteins (REMAP), useful for
PT diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or
PT infections.

XX PS Claim 1; SEQ ID NO 19; 298pp; English.

XX CC The invention relates to a novel isolated polypeptide comprising a human
CC receptor and membrane-associated protein (REMAP). The polypeptide of the
CC invention demonstrates cytostatic, antiarteriosclerotic, anticonvulsant,
CC nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
CC antiinflammatory and thromimetic activities and may be useful for
CC treating and diagnosing various disorders including those which are cell
CC proliferative such as cancer and atherosclerosis, neurological including
CC epilepsy, Huntington's disease and stroke, immune/inflammatory
CC and particularly AIDS and allergies and developmental such as hypothyroidism
CC and Cushing's syndrome, as well as infections. The current sequence is
CC that of the human REMAP protein of the invention.

XX SQ Sequence 172 AA;

Query Match 100.0%; Score 116; DB 7; Length 172;
Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ov 1 KENSAPFPCCNDNVNTAN 20
|||||
Db 96 KENSAPFPCCNDNVNTAN 115

RESULT 10

ADP81123
ID ADP81123 standard; protein; 174 AA.

XX AC ADP81123;

XX DT 09-SEP-2004 (first entry)

XX DE Protein of human ovarian specific gene, SEQ ID No 157.

XX DE normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;
KW metastatic; cancer; vaccine; cytostatic; human.

XX OS Homo sapiens.

XX PN W02004053079-A2.

XX PD 24-JUN-2004.

XX PF 08-DEC-2003; 2003WO-US038855.

XX PR 06-DEC-2002; 2002US-0431301P.

XX PR 30-JUN-2003; 2003US-0484584P.

XX PR 07-NOV-2003; 2003US-0518607P.

XX PA (DIAD-) DIADEXUS INC.

XX PI Macina RA, Turner LR, Sun Y, Liu S, Chen H;

XX WPI; 2004-468850/44.

XX DR N-PSDB; ADP80988.

XX PT New ovarian specific nucleic acid molecules and polypeptides useful for
PT diagnosing, preventing or treating ovarian cancer, for producing
PT transgenic animals or cells, or for research purposes.

XX PS Claim 12; SEQ ID NO 157; 754pp; English.

XX CC The invention relates to novel isolated nucleic acid molecules and
CC polypeptides present in normal and neoplastic ovarian cells. These
CC comprise a nucleic acid sequence encoding any of the 167 amino acid
CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
CC specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
CC in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
CC further comprises: a method for determining the presence of a ovarian
CC specific nucleic acid (OSNA) in a sample; a vector comprising the above
CC nucleic acid molecule; a host cell comprising the vector; a method for
CC producing a polypeptide encoded by the above nucleic acid molecule; a
CC polypeptide encoded by the nucleic acid molecule cited above; an antibody
CC or its fragment that specifically binds to the above polypeptide; a
CC method for determining the presence of an ovarian specific protein in a
CC sample; a method for diagnosing or monitoring the presence and metastases
CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or
CC presence of cancer in a patient; the kit comprising a means for
CC determining the presence of the above nucleic acid molecule or
CC polypeptide; a method of treating a patient with ovarian cancer; and a
CC vaccine comprising the above polypeptide or nucleic acid encoding the
CC polypeptide. The isolated nucleic acid molecules and polypeptides have
CC cytostatic activity. The isolated polypeptides may be used to create a
CC vaccine. The isolated nucleic acid molecules and polypeptides can be used
CC for diagnosing or monitoring the presence and metastases of ovarian
CC cancer and treating ovarian cancer. This sequence represents the protein
CC of an ovarian specific gene of the invention.

XX SQ Sequence 174 AA;

Query Match 100.0%; Score 116; DB 8; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNSAFPPPCNDNVNTAN 20
|||||
DB 53 KNSAFPPPCNDNVNTAN 72
|||||

RESULT 11
ADR65994
ID ADR65994 standard; protein; 214 AA.
XX
AC ADR65994;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived protein SEQ ID 190 #1.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis.
XX
OS Homo sapiens.
XX
FN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Xinzhong L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
XX Claim 2; Page 585; 1607pp; German.

This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated

CC sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the invention.

SQ Sequence 214 AA;
Query Match 100.0%; Score 116; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNSAFPPPCNDNVNTAN 20
|||||
DB 138 KNSAFPPPCNDNVNTAN 157
|||||

RESULT 12
ADR66892
ID ADR66892 standard; protein; 214 AA.
XX
AC ADR66892;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived DNA SEQ ID 190 #4.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis.
XX
OS Homo sapiens.
XX
FN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Xinzhong L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
XX Claim 2; Page 1545; 1607pp; German.

This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular

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us-09-780-669-114_copy_165_184.rag

CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies:
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR5805-ADR6954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.

XX Sequence 214 AA;

Query Match 100.0%; Score 116; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSARPPFCNDNVNTAN 20
Db 138 KENSARPPFCNDNVNTAN 157
|||||

RESULT 13
AAW75060
ID AAW75060 standard; protein; 233 AA.

XX AAW75060;

25-MAR-2003 (revised)
28-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 4 clone HKCSR70.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; fetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Misc-difference 233 /label= unknown
FT FT

XX WO9839446-A2.

XX 11-SEP-1998.

XX 06-MAR-1998; 98WO-US004482.

XX 07-MAR-1997; 97US-0038621P.

XX 07-MAR-1997; 97US-0040161P.

XX 07-MAR-1997; 97US-0040162P.

XX 07-MAR-1997; 97US-0040163P.

XX 07-MAR-1997; 97US-0040333P.

XX 07-MAR-1997; 97US-0040334P.

XX 07-MAR-1997; 97US-0040336P.

XX 11-APR-1997; 97US-0043311P.

PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-00433568P.
PR 11-APR-1997; 97US-00433576P.
PR 11-APR-1997; 97US-00433578P.
PR 11-APR-1997; 97US-00433580P.
PR 11-APR-1997; 97US-00433689P.
PR 11-APR-1997; 97US-00433670P.
PR 11-APR-1997; 97US-00433671P.
PR 11-APR-1997; 97US-00433672P.
PR 11-APR-1997; 97US-00433674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.

PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057761P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JW;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI; 1998-609887/51.
DR N-PSDB; AAV34157.
XX
XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
XX Claim 1; Page 281-282; 447pp; English.
XX
XX This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAV34145) for increasing the stability of the fused protein
CC as compared to the human protein only. The invention relates to 70 novel
CC genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino
CC acid sequences AAW5057-W5179) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 70 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 233 AA;

Query Match 100.0%; Score 116; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPFCNDNVNTAN 20
| | | | | | | | | | | | | | | | | | | | | |
Db 156 KENSAPPPFCNDNVNTAN 175

RESULT 14
ABO01936
ID ABO01936 standard; protein; 233 AA.
XX
XX ABO01936;
AC
XX
XX 12-AUG-2003 (first entry)
DT
XX
XX Novel human secreted protein #4.
XX
XX Human; immunoglobulin G; IgG; fragment of crystallisation; Fc;
KW immune system disorder; haematopoietic cell disorder;
KW immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
KW Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
KW blood coagulation disorder; blood platelet disorder; autoimmune disorder;
KW Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW glomerulonephritis; Grave's disease; allergic reaction;
KW graft-versus-host disease; hyperproliferative disorder; neoplasm;
KW infectious disease; nervous system disease; spinal cord disorder;

KW head trauma; stroke; tissue regeneration; congenital defect; trauma;
KW wound; burn; incision; ulcer; age disease; osteoporosis;
KW periodontal disease; liver failure; catabolism; anabolism; metabolism;
KW food additive; preservative; secreted protein.
XX
XX Homo sapiens.
XX
XX US2003027132-A1.
XX
XX 06-FEB-2003.
XX
XX 04-SEP-1998; 98US-00148545.
XX
XX 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.

PR 22-AUG-1997; 97US-0056632P.
 PR 22-AUG-1997; 97US-0056636P.
 PR 22-AUG-1997; 97US-0056637P.
 PR 22-AUG-1997; 97US-0056662P.
 PR 22-AUG-1997; 97US-0056664P.
 PR 22-AUG-1997; 97US-0056684P.
 PR 22-AUG-1997; 97US-0056862P.
 PR 22-AUG-1997; 97US-0056864P.
 PR 22-AUG-1997; 97US-0056872P.
 PR 22-AUG-1997; 97US-0056874P.
 PR 22-AUG-1997; 97US-0056875P.
 PR 22-AUG-1997; 97US-0056876P.
 PR 22-AUG-1997; 97US-0056877P.
 PR 22-AUG-1997; 97US-0056878P.
 PR 22-AUG-1997; 97US-0056879P.
 PR 22-AUG-1997; 97US-0056880P.
 PR 22-AUG-1997; 97US-0056881P.
 PR 22-AUG-1997; 97US-0056882P.
 PR 22-AUG-1997; 97US-0056884P.
 PR 22-AUG-1997; 97US-0056886P.
 PR 22-AUG-1997; 97US-0056887P.
 PR 22-AUG-1997; 97US-0056888P.
 PR 22-AUG-1997; 97US-0056889P.
 PR 22-AUG-1997; 97US-0056892P.
 PR 22-AUG-1997; 97US-0056893P.
 PR 22-AUG-1997; 97US-0056894P.
 PR 22-AUG-1997; 97US-0056903P.
 PR 22-AUG-1997; 97US-0056908P.
 PR 22-AUG-1997; 97US-0056909P.
 PR 22-AUG-1997; 97US-0056910P.
 PR 22-AUG-1997; 97US-0056911P.
 PR 03-SEP-1997; 97US-0057650P.
 PR 06-MAR-1998; 98WO-US004482.
 XX
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (TISC/) FISCHER C L.
 PA (SOPP/) SOPPET D R.
 PA (CART/) CARTER K C.
 PA (BEDN/) BEDNARIK D R.
 PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.
 PA (FENG/) FENG P.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (DUAN/) DUAN R.
 PA (HULJ/) HU J.
 PA (FLOR/) FLORENCE K A.
 PA (OLSE/) OLSEN H S.
 PA (EBNE/) EBNER R.
 PA (BREW/) BREWER L A.
 PA (SHIY/) SHI Y.
 XX
 PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
 PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
 PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA,
 PI Shi Y;
 XX
 WIPI; 2003-466138/44.
 DR N-PSDB; ACD08028.
 XX
 Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing
 PT or treating deficiencies or disorders of the immune system, autoimmune
 PT disorders, hyperproliferative disorders, and infectious diseases.
 XX
 PS Claim 11; Page 173; 243pp; English.
 CC
 XX The invention describes an isolated human secreted HODAZ50 polypeptide
 CC (I) comprising a sequence at least 95% identical to a sequence selected
 CC from polypeptide fragment of any one of the 123 polypeptide sequences

CC (PS) fully defined in the specification and having biological activity,
 CC polypeptide domain or epitope of PS, secreted form of PS, full-length
 CC protein of PS, or variant, allelic variant or species homologue of PS.
 CC (I) or a polynucleotide (II) encoding (I) is useful for preventing,
 CC treating, or ameliorating a medical condition in a mammalian subject. (I)
 CC or (II) is also useful for diagnosing a pathological condition or a
 CC susceptibility to a pathological condition in a subject. (I) is useful
 CC for identifying a binding partner which involves contacting the
 CC polypeptide with the binding partner and determining whether the binding
 CC partner affects the activity of the polypeptide. (I) or (II) is useful
 CC for diagnosing or treating deficiencies or disorders of the immune
 CC system, deficiencies or disorders of haematopoietic cells, to treat
 CC immunologic deficiency disorders, ataxia telangiectasia, HIV infection,
 CC Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood
 CC coagulation disorders, blood platelet disorders, autoimmune disorders
 CC (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis,
 CC dermatitis, glomerulonephritis, Grave's disease), allergic reactions,
 CC graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms,
 CC located in the abdomen, bone, breast, digestive system, liver, pancreas,
 CC peritoneum, endocrine glands), infectious diseases (e.g., viral,
 CC bacterial, fungal or parasitic infection), central and peripheral nervous
 CC system diseases (e.g., spinal cord disorders, head trauma or stroke), to
 CC differentiate, proliferate and attract cells leading to the regeneration
 CC of tissues to repair, replace or protect tissue damaged by congenital
 CC defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g.,
 CC osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV)
 CC is useful to modulate mammalian characteristics, to modulate mammalian
 CC metabolism affecting catabolism, anabolism, processing, utilisation, and
 CC storage of energy, to change a mammal's mental state or physical state,
 CC or as a food additive or preservative, such as to increase or decrease
 CC storage capabilities, fat content, lipid, protein, carbohydrate,
 CC vitamins, minerals, cofactors or other nutritional components. This is
 CC the amino acid sequence of a novel human secreted protein
 XX
 SQ Sequence 233 AA;

Query Match 100.0%; Score 116; DB 6; Length 233;

Best Local Similarity 100.0%; Pred. No. 4.8e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KENSAPPPPCNDNVNTNAN 20

DB 156 KENSAPPPPCNDNVNTNAN 175

RESULT 15

AAG62153

ID AAG62153 standard; protein; 240 AA.

XX

AC AAG62153;

XX 06-JUL-2001 (first entry)

DT

XX Human P503S inventive antigen SEQ ID NO: 352.

DE

XX Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;
 KW chromosome 11p13; zinc finger transcription factor.
 XX Homo sapiens.
 OS WO200125273-A2.
 XX 12-APR-2001.
 XX 04-OCT-2000; 2000WO-US027465.
 XX 04-OCT-1999; 99US-0157459P.
 XX (CORI-) CORIXA CORP.
 XX Skeiky YAW, Xu J, Cheever MA, Reed SG;
 XX WPI; 2001-328324/34.

XX Polypeptide comprising part of the Wilms Tumor gene product sequence is
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
 PT and cancer associated with WT1.
 XX
 PS Disclosure; Page 223-224; 228pp; English.
 XX
 CC The present invention describes compositions comprising peptides derived
 CC from the Wilm's tumour protein WT1 and methods for their use in treating
 CC malignant diseases. Peptides derived from both the murine and human WT1
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
 CC and the protein was shown to be a zinc finger transcription factor. The
 CC immunogenic peptides of the invention are particularly useful in the
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is
 CC a polypeptide described in the exemplification of the invention
 XX
 SQ Sequence 240 AA;

Query Match 100.0%; Score 116; DB 4; Length 240;
 Best Local Similarity 100.0%; Pred. No. 5e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KENSAPPPFCNDNVNTAN 20
 |||||
 Db 165 KENSAPPPFCNDNVNTAN 184

Search completed: February 5, 2005, 19:59:55
 Job time : 104.746 secs

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	116	100.0	20	9	US-09-759-143-505	Sequence 505, App	
2	116	100.0	20	9	US-09-780-669-505	Sequence 505, App	
3	116	100.0	20	9	US-09-822-827-505	Sequence 505, App	
4	116	100.0	20	9	US-09-895-793-505	Sequence 505, App	
5	116	100.0	20	9	US-09-895-814-505	Sequence 505, App	
6	116	100.0	20	13	US-10-013-896-505	Sequence 505, App	
7	116	100.0	20	14	US-10-010-940-505	Sequence 505, App	
8	116	100.0	20	14	US-10-144-678A-505	Sequence 505, App	
9	116	100.0	20	14	US-10-294-095-505	Sequence 505, App	
10	116	100.0	233	9	US-09-981-876-137	Sequence 137, App	
11	116	100.0	233	10	US-09-148-545-137	Sequence 137, App	
12	116	100.0	240	15	US-10-264-237-1489	Sequence 1489, App	
13	116	100.0	241	9	US-09-759-143-114	Sequence 114, App	

Query Match 100.0%; Score 116; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPCCNDNVNTAN 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KENSAPPPCCNDNVNTAN 20

RESULT 2
US-09-780-669-505
; Sequence 505, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-780-669-505

Query Match 100.0%; Score 116; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPCCNDNVNTAN 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KENSAPPPCCNDNVNTAN 20

RESULT 3
US-09-822-827-505
; Sequence 505, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505

; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-822-827-505

Query Match 100.0%; Score 116; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPCCNDNVNTAN 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KENSAPPPCCNDNVNTAN 20

RESULT 4
US-09-895-793-505
; Sequence 505, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-895-793-505

Query Match 100.0%; Score 116; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPCCNDNVNTAN 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 KENSAPPPCCNDNVNTAN 20

RESULT 5
US-09-895-814-505
; Sequence 505, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

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; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-895-814-505

Query Match      100.0%; Score 116; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KENSAPPPFCNDNVNTAN 20
      |||
Db      1 KENSAPPPFCNDNVNTAN 20
      |||

RESULT 6
US-10-012-896-505
; Sequence 505, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
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; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-012-896-505

Query Match      100.0%; Score 116; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KENSAPPPFCNDNVNTAN 20
      |||
Db      1 KENSAPPPFCNDNVNTAN 20
      |||

RESULT 7
US-10-010-940-505
; Sequence 505, Application US/10010940
; Publication No. US20030089062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-010-940-505

Query Match      100.0%; Score 116; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KENSAPPPFCNDNVNTAN 20
      |||
Db      1 KENSAPPPFCNDNVNTAN 20
      |||

RESULT 8
US-10-144-678A-505
; Sequence 505, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
```

```

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRI
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-144-678A-505

Query Match 100.0%; Score 116; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KENSAFPFFCCNDNVNTAN 20
Db 1 KENSAFPFFCCNDNVNTAN 20

RESULT 9
US-10-294-025-505
; Sequence 505, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRI
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-294-025-505

Query Match 100.0%; Score 116; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KENSAFPFFCCNDNVNTAN 20
Db 1 KENSAFPFFCCNDNVNTAN 20

RESULT 10
US-09-981-876-137
; Sequence 137, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US/09/981,876
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632
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;
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
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; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233

Query Match 100.0%; Score 116; DB 9; Length 233;

Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPFCNDNVNTAN 20
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Db 156 KENSAPPPFCNDNVNTAN 175

RESULT 11
US-09-148-545-137
; Sequence 137, Application US/09148545

Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
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EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 137
LENGTH: 233

Query Match 100.0%; Score 116; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 156 KENSAPPPFCNDNVNTAN 175

RESULT 12
US-10-264-237-1489
Sequence 1489, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P413P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1489
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-237-1489

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RESULT 13
US-09-759-143-114
Sequence 114, Application US/09759143
Patent No. US200202248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 114
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapien
US-09-759-143-114

Query Match 100.0%; Score 116; DB 9; Length 241;
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Qy 1 KENSAPPPFCNDNVNTAN 20
Db 165 KENSAPPPFCNDNVNTAN 184

RESULT 14
US-09-780-669-114
Sequence 114, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.

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; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-780-669-114

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Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-114

Query Match      100.0%; Score 116; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      165 KENSAPPPFCCNDNVNTAN 184

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Job time : 75.9153 secs
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Query Match      100.0%; Score 116; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      165 KENSAPPPFCCNDNVNTAN 184

RESULT 15
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; Sequence 114, Application US/09030606
; Patent No. US20020081590A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:49:45 ; Search time 19.661 Seconds
(without alignments)
97.876 Million cell updates/sec

Title: US-09-780-669-114_COPY_165_184
Perfect score: 116
Sequence: 1 KENSAPPPFCNDNVNTAN 20
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	51	44.0	860	1 VCLJ84	env polyprotein pr
4	50	43.1	301	2 S75391	probable methionyl
5	50	43.1	566	2 S19307	carboxylesterase (
6	48	41.4	1293	2 S42402	xeroderma pigmento
7	46	39.7	194	2 F64598	modulator of drug
8	46	39.7	633	2 T04179	hypothetical prote
9	46	39.7	859	1 VCLJ72	env polyprotein pr
10	46	39.7	859	1 VCLJ81	env polyprotein pr
11	46	39.7	859	1 VCLJ82	env polyprotein pr
12	46	39.7	859	1 VCLJ83	env polyprotein pr
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25	44	37.9	996	2 S70646	transcription fact
26	43	37.1	68	2 AB0417	conserved hypothet
27	43	37.1	194	2 A71915	hypothetical prote
28	43	37.1	241	2 S42436	proteasome endopep
29	43	37.1	304	2 S12975	coat protein - pot

ALIGNMENTS

RESULT 1

A59262
tetraspan TSPAN-1 - human
C:Species: Homo sapiens (man)
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59262
R: Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A:Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.
A:Reference number: A59258; MUID:98390278; PMID:9714763
A:Accession: A59262
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-241 <TOD>
A:Cross-references: UNIPROT:O60635; GB:AF054838; NID:G2997740; PIDN:AAC69714.1; PID:G2999
C:Genetics:
A:Gene: TSPAN-1
C:Superfamily: CD9 antigen

Query Match 100.0%; Score 116; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPFCNDNVNTAN 20
||| ||||| ||||| ||||| |||||
Db 165 KENSAPPPFCNDNVNTAN 184

RESULT 2

A46222
hydrophobin Ccg-2 - Neurospora crassa
N:Alternate names: blue-light-inducible protein bli-7
C:Species: Neurospora crassa
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46222; A56645
R: Bell-Pedersen, D.; Dunlap, J.C.; Loros, J.J.
Genes Dev. 6, 2382-2394, 1992
A:Title: The Neurospora circadian clock-controlled gene, ccg-2, is allelic to eas and en and
A:Reference number: A46222; MUID:93093472; PMID:1459460
A:Accession: A46222
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <BEL>
A:Cross-references: UNIPROT:Q04571; GB:X67339; GB:SS0953; NID:G29983; PIDN:CAA47754.1; PI:
R:Eberle, J.; Russo, V.E.
DNA Seq. 3, 131-141, 1992
A:Title: Neurospora crassa blue-light-inducible gene bli-7 encodes a short hydrophobic p
A:Reference number: A56645; MUID:93112994; PMID:1472707
A:Accession: A56645
A:Molecule type: DNA
A:Residues: 1-108 <EBE>

A:Residues: 1-301 <SEN>
A:Cross-references: UNIPROT:P95963; EMBL:Y08257; NID:gl107772; PIDN:CAR69553.1; PID:G1170
A:Experimental source: strain p2
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C:Superfamily: Escherichia coli methionyl aminopeptidase
C:Keywords: aminopeptidase

2

```
RESULT 7
F64598
modulator of drug activity - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: F64598
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, G.G.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 368, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: F64598
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-194 <TM>
A:Cross-references: UNIPROT:O25347; GB:AE000577; GB:AE000511; NID:g2313747; PIDN:AA0769
C:Superfamily: NAD(P)H dehydrogenase (quinone) 2

Query Match          39.7%; Score 46; DB 2; Length 194;
Best Local Similarity 64.3%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 SAPPFPCNDNVN 17
Db 161 SALPTFCNDVVKN 174

RESULT 8
T04179
hypothetical protein F7L13.20 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04179
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15184
A:Accession: T04179
A:Molecule type: DNA
A:Residues: 1-633 <BEV>
A:Cross-references: UNIPROT:Q9S2X8; EMBL:AL049524
A:Experimental source: cultivar Columbia; BAC clone F7L13
C:Genetics:
A:Map position: 4
A:Introns: 224/3; 295/1; 394/2; 550/2
A>Note: F7L13.20

Query Match          39.7%; Score 46; DB 2; Length 633;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KENSAPPFPCNDN 14
Db 376 KONNKSPPICSDN 389

RESULT 9
VCLJ22
env polypeptide precursor - equine infectious anemia virus (strain CL22)
N:Alternate names: coat polypeptide
N:Contains: coat protein gp45; coat protein gp90
C:Species: equine infectious anemia virus
A>Note: host Equus caballus (domestic horse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: C41991
R:Perry, S.T.; Flaherty, M.T.; Kelley, M.J.; Clabough, D.L.; Tronick, S.R.; Coggins, L.;
J. Virol. 66, 4085-4097, 1992
A>Title: The surface envelope protein gene region of equine infectious anemia virus is r
A:Reference number: A41991; MUID:92292230; PMID:1318398
A:Accession: C41991
```

```
A:Molecule type: DNA
A:Residues: 1-859 <PER>
A:Cross-references: UNIPROT:P32541; GB:MB7581; NID:g290627; PIDN:AAA43005.1; PID:g290630
C:Genetics:
A:Gene: env
C:Superfamily: equine infectious anemia virus env polypeptide
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-859/Product: env polypeptide #status predicted <ENV>
F:23-444/Product: coat protein gp90 #status predicted <GP>
F:445-859/Product: coat protein gp45 #status predicted <GP>
F:446-472/Region: hydrophobic
F:615-636/Domain: transmembrane #status predicted <TM>
F:40,112,141,148,186,214,233,244,340,368,399,406,411,483,490,550,557/Binding site: carbo
Query Match          39.7%; Score 46; DB 1; Length 859;
Best Local Similarity 38.9%; Pred. No. 48;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KENSAPPFPCNDNVNT 18
Db 28 EENTMFQPCYNNDKNS 45

RESULT 10
VCLJE1
env polypeptide precursor (clone P3.2-1) - equine infectious anemia virus
N:Contains: coat protein gp45; coat protein gp90
C:Species: equine infectious anemia virus
A>Note: host Equus caballus (domestic horse)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A34027
R:Payne, S.L.; Fang, F.D.; Liu, C.P.; Dhruva, B.R.; Rambo, P.; Issel, C.J.; Montelaro,
Virology 161, 321-331, 1987
A>Title: Antigenic variation and lentivirus persistence: variations in envelope gene seq
A:Reference number: A34027; MUID:88072070; PMID:2825406
A:Accession: A34027
A:Molecule type: genomic RNA
A:Residues: 1-859 <PAV>
A:Cross-references: UNIPROT:P22427; GB:M18385; NID:g323830; PIDN:AAA66407.1; PID:g323831
C:Genetics:
A:Gene: env
C:Superfamily: equine infectious anemia virus env polypeptide
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-444/Product: coat protein gp90 #status predicted <CP1>
F:75-93/Domain: transmembrane #status predicted <TM1>
F:445-859/Product: coat protein gp45 #status predicted <CP2>
F:446-462/Domain: transmembrane #status predicted <TM2>
F:614-636/Domain: transmembrane #status predicted <TM3>
F:787-807/Domain: transmembrane #status predicted <TM4>
F:816-835/Domain: transmembrane #status predicted <TM5>
F:40,112,141,148,186,214,233,244,340,368,399,406,411,422,483,490,550,557,752/Binding sit
Query Match          39.7%; Score 46; DB 1; Length 859;
Best Local Similarity 38.9%; Pred. No. 48;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KENSAPPFPCNDNVNT 18
Db 28 EENTMFQPCYNNDKNS 45

RESULT 11
VCLJE2
env polypeptide precursor (clone P3.2-2) - equine infectious anemia virus
N:Contains: coat protein gp45; coat protein gp90
C:Species: equine infectious anemia virus
A>Note: host Equus caballus (domestic horse)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: B34027
R:Payne, S.L.; Fang, F.D.; Liu, C.P.; Dhruva, B.R.; Rambo, P.; Issel, C.J.; Montelaro,
Virology 161, 321-331, 1987
```

[illegible]

RESULT 15
VCLJWS
env polypotein precursor - equine infectious anemia virus (strain WSUS)
N:Contains: coat protein gp45; coat protein gp90
C:Species: equine infectious anemia virus
A:Note: host Equus caballus (domestic horse)

C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C:Accession: S07589
 R:McGuire, T.C.; Lacy, P.A.; O'Rourke, K.I.
 Nucleic Acids Res. 18, 196, 1990
 A:Title: cDNA sequence of the env gene of a pathogenic equine infectious anemia lentivirus
 A:Reference number: S07589; MUID:90174929; PMID:2155398
 A:Accession: S07589
 A>Status: translation not shown
 A:Molecule type: genomic RNA
 A:Residues: 1-859 <MCG>
 A:Cross-references: UNIPROT:P16082; EMBL:X16988; NID:G59246; PIDN:CRA34856.1; PID:G59247
 C:Genetics:
 A:Gene: env
 C:Superfamily: equine infectious anemia virus env polypeptide
 C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-44/Product: coat protein gp90 #status predicted <GP1>
 F:75-93/Domain: transmembrane #status predicted <TM1>
 F:445-859/Product: coat protein gp45 #status predicted <GP2>
 F:446-462/Domain: transmembrane #status predicted <TM2>
 F:614-636/Domain: transmembrane #status predicted <TM3>
 F:787-807/Domain: transmembrane #status predicted <TM4>
 F:816-835/Domain: transmembrane #status predicted <TM5>
 F:40,112,141,148,186,214,233,244,313,340,368,399,406,411,483,490,550,557,752/Binding site

Query Match 39.7%; Score 46; DB 1; Length 859;
 Best Local Similarity 38.9%; Pred. NO. 48;
 Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 1 KENSAFPFPCGNDVNT 18
 Db 28 EENTMFQPCYNDSKNS 45

Search completed: February 5, 2005, 20:05:45
 Job time : 20.661 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:36:20 ; Search time 94.9153 Seconds
(without alignments)
107.902 Million cell updates/sec

Title: US-09-780-669-114_COPY_165_184

Perfect score: 116

Sequence: 1 KENSAFPFPCCNDNVNTAN 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	241	1	TSN1_HUMAN
2	65	56.0	241	2	Q6AYR9
3	53	45.7	282	2	Q86FC1
4	51	44.0	91	2	Q6J758
5	51	44.0	91	2	Q6J763
6	51	44.0	91	2	Q6J766
7	51	44.0	91	2	Q6J767
8	51	44.0	91	2	Q6J768
9	51	44.0	91	2	Q6J769
10	51	44.0	108	1	RODL_NEUCR
11	51	44.0	860	1	ENV_EFV5
12	51	44.0	863	2	Q6AXF9
13	51	44.0	923	2	Q1X64
14	50	43.1	91	2	Q6J765
15	50	43.1	240	2	Q9J759
16	50	43.1	301	1	AMPM_SULSO
17	50	43.1	489	2	Q651F0
18	50	43.1	565	2	Q97582
19	50	43.1	566	1	EST1_PIG
20	49.5	42.7	850	2	Q70014
21	49	42.2	91	1	NLT1_PRUDU
22	48	41.4	810	2	Q6NBT3
23	48	41.4	888	2	Q6LST1
24	48	41.4	1293	1	XPC_DROME
25	48	41.4	1293	2	Q9U321
26	48	41.4	1293	2	Q9V7A8
27	48	41.4	1294	2	Q8MLA2
28	48	41.4	1623	2	Q7PDV5
29	47	40.5	297	2	Q6QW78
30	47	40.5	375	2	Q6EH13
31	46	39.7	66	2	Q66747

32	46	39.7	74	2	Q85499
33	46	39.7	90	2	Q8H2B2
34	46	39.7	91	1	NLT1_PRUAR
35	46	39.7	91	1	NLT1_PRUPE
36	46	39.7	91	2	Q9LED1
37	46	39.7	117	1	NLT1_PRUDU
38	46	39.7	123	2	Q6Z9S7
39	46	39.7	194	2	O25347
40	46	39.7	234	2	P88309
41	46	39.7	234	2	P88310
42	46	39.7	234	2	P88311
43	46	39.7	234	2	P88316
44	46	39.7	248	2	P88312
45	46	39.7	248	2	P88313

ALIGNMENTS

RESULT 1
TSN1_HUMAN
ID TSN1_HUMAN STANDARD; PRT; 241 AA.
AC O60635; O60745;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tetraspanin 1 (Tspan-1) (Tetraspanin NET-1) (Tetraspanin TM4-C).
GN Name=TSpan1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9839278; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6;
RA Todd S.C., Doctor V.S., Levy S.;
RT "Sequences and expression of six new members of the tetraspanin/TM4SF family.";
RL Biochim. Biophys. Acta 1399:101-104(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Rubinstein E., Serru V., Boucheix C.;
RT "New tetraspans identified in the EST database.";
RN [3]
RP SEQUENCE FROM N.A.
RA Puls K.L., Ni J., Liu D., Morahan G., Wright M.D.;
RT "The molecular characterization of four tetraspans.";
RN [4]
RP SEQUENCE FROM N.A.
RA TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Q85499	equine infe
Q8H2B2	prunus pers
P81651	prunus arme
P81402	prunus pers
Q9LED1	prunus pers
Q43017	prunus dulc
Q6Z9S7	Oryza sativ
O25347	helicobacte
P88309	human immun
P88310	human immun
P88311	human immun
P88316	human immun
P88312	human immun
P88313	human immun

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF054838; AAC69714.1; -
CC EMBL: AF065388; AAC17119.1; -
CC EMBL: AF133425; AAF08364.1; -
CC EMBL: BC007290; AAH07290.1; -
CC EMBL: BC013404; AAH13404.1; -
CC PIR: A59262; A59262.
CC H-InvDB: HIX0000543; -
CC GO: GO:0016021; C: integral to membrane; TAS.
CC InterPro: IPR008952; Tetraspanin.
CC InterPro: IPR000301; Transmem_4.
CC Pfam: PF00335; Tetraspanin; 1.
CC PRINTS: PR00259; TMFOUR.
CC PROSITE: PS00421; TM4.1; FALSE_NEG.
KW Glycoprotein; Transmembrane.
FT DOMAIN 1 11
FT TRANSMEM 12 32 Cytoplasmic (Potential).
FT DOMAIN 33 52 Potential.
FT TRANSMEM 53 73 Extracellular (Potential).
FT DOMAIN 74 88 Potential.
FT TRANSMEM 89 109 Cytoplasmic (Potential).
FT DOMAIN 110 211 Extracellular (Potential).
FT TRANSMEM 212 232 Potential.
FT DOMAIN 233 241 Cytoplasmic (Potential).
FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 154 154 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CONFLICT 189 189 K -> E (in Ref. 1).
SQ SEQUENCE 241 AA; 26301 MW; AF938AD7147CB884 CRC64;

Query Match 100.0%; Score 116; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPCCNDNVNTAN 20
Db 165 KENSAPPPCCNDNVNTAN 184
|||||

RESULT 2
Q6AYR9 PRELIMINARY; PRT; 241 AA.
AC Q6AYR9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tetraspanin 1.
GN Name:MGCS3753;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC078938; AAH78938.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR InterPro: IPR002229; RhesusRHD.
DR InterPro: IPR008952; Tetraspanin.
DR InterPro: IPR000301; Transmem_4.
DR Pfam: PF00335; Tetraspanin; 1.
DR PRINTS: PR00342; RhesusRHD.
DR PRINTS: PR00259; TMFOUR.
DR PROSITE: PS00421; TM4.1; 1.
SQ SEQUENCE 241 AA; 26453 MW; 9118E865464D1A70 CRC64;

Query Match 56.0%; Score 65; DB 2; Length 241;
Best Local Similarity 71.4%; Pred. No. 0.043;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KENSAPPPCCNDN 14
Db 165 KENSAPPPCCANN 178
|||||

RESULT 3
Q86FC1 PRELIMINARY; PRT; 282 AA.
AC Q86FC1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Clone ZD391 mRNA sequence.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
RA Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
RA Xue C.L., Peng Z., Chen Z., Han Z.G.;
RT "Evolutionary and biomedical implications of a Schistosoma japonicum
RT complementary DNA resource.";
RL Nat. Genet. 35:139-147 (2003).
DR EMBL: AY222942; AAP05954.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR InterPro: IPR000301; Transmem_4.
DR Pfam: PF00335; Tetraspanin; 1.
SQ SEQUENCE 282 AA; 31153 MW; 6CB2B4D2ED2B37C4 CRC64;

Query Match 45.7%; Score 53; DB 2; Length 282;
Best Local Similarity 66.7%; Pred. No. 3.9;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 NSAPPPCCNDN 14
|||||

Query Match	44.0%	Score 51;	DB 2;	Length 91;
Best Local Similarity	72.7%	Pred. No. 2.5;		

[illegible]

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC079573; AAH79573.1; -
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00084; Sushi; 5.
 DR SMART; SM00032; CCP; 5.
 DR SMART; SM00042; CUB; 3.
 DR PROSITE; PS01180; CUB; 3.
 DR PROSITE; PS50923; SUSHI; 5.
 SQ SEQUENCE 863 AA; 93371 MW; 82AC231639C0EB75 CRC64;
 Query Match 44.0%; Score 51; DB 2; Length 863;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KENSAPPPFCNDVNTVT 18
 Db 400 EEDRCPPFLAHGNVTT 417
 RESULT 13
 Q91X64
 ID Q91X64 PRELIMINARY; PRT; 923 AA.
 AC Q91X64;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Seizure related 6 homolog (Mouse)-like 2 (Mus musculus adult male
 DE diencephalon cDNA, RIKEN full-length enriched library,
 DE clone:933015G34 product:TYPE I TRANSMEMBRANE RECEPTOR homolog).
 GN Name=Sez612;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RA Strausberg R.J.
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA The FANTOM Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saichon H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011475; AAH11475.1; -
 DR EMBL; AK034088; BAC28579.1; -
 DR HSSP; P08174; INNW.
 DR MGI; MGI:2385295; Sez612.

RL Genome Res. 10:1757-1771(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Iehi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamanura T., Yamanaka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003448; AAH03448.1; -.
DR EMBL; AK078869; BAC37431.1; -.
DR MGD; MGI:1914055; 9030418M05Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00342; RHEUSRHD.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
SQ SEQUENCE 240 AA; 26356 MW; AD4C48A32BC2999 CRC64;

Query Match 43.1%; Score 50; DB 2; Length 240;
Best Local Similarity 72.7%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KENSAPPPFCC 11
Db ||| ||| |||
165 KENKVFPPCC 175

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